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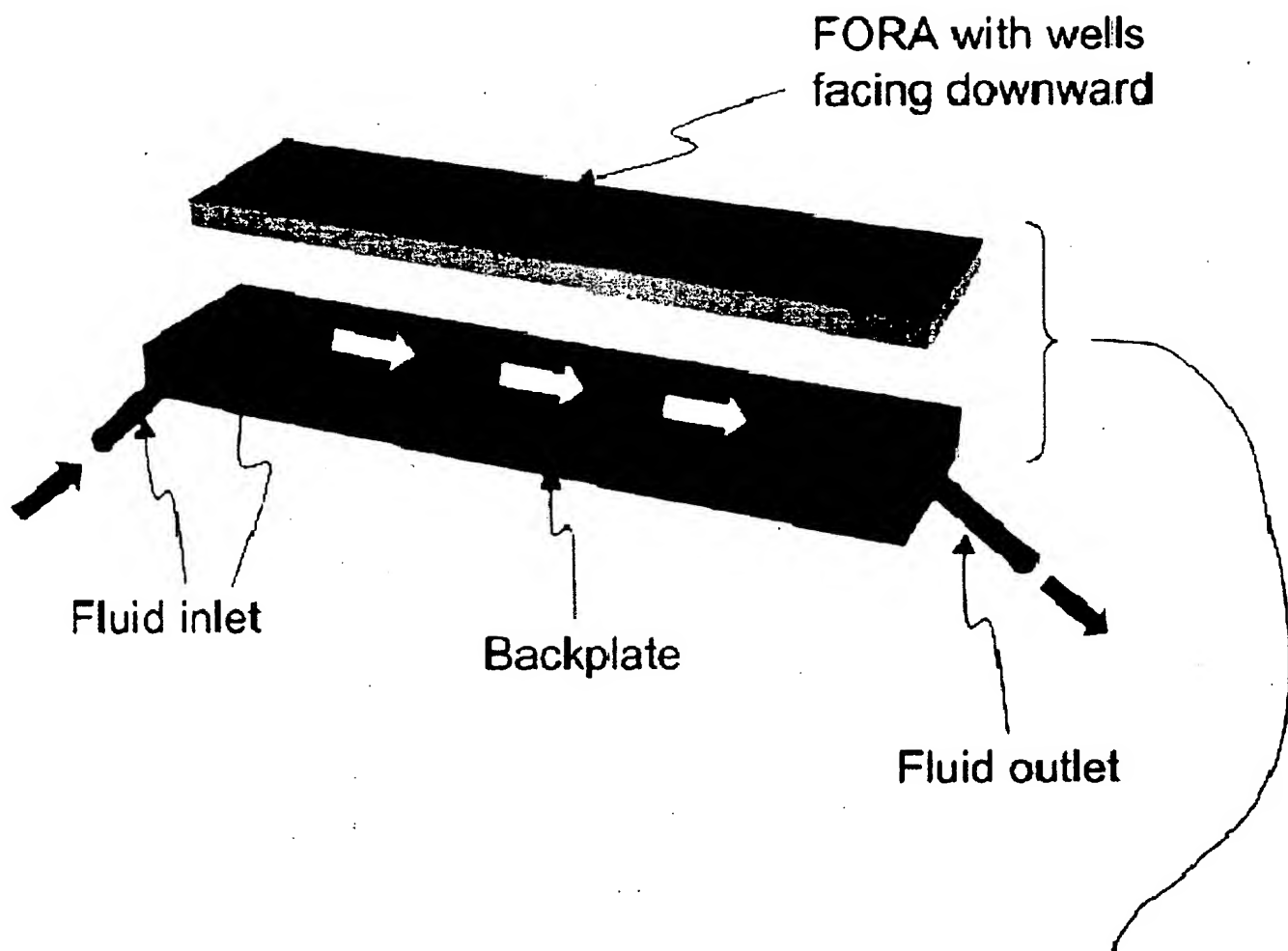
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FORA and back-plate are pressed together with a seal to create a closed flow chamber.

Figure 16

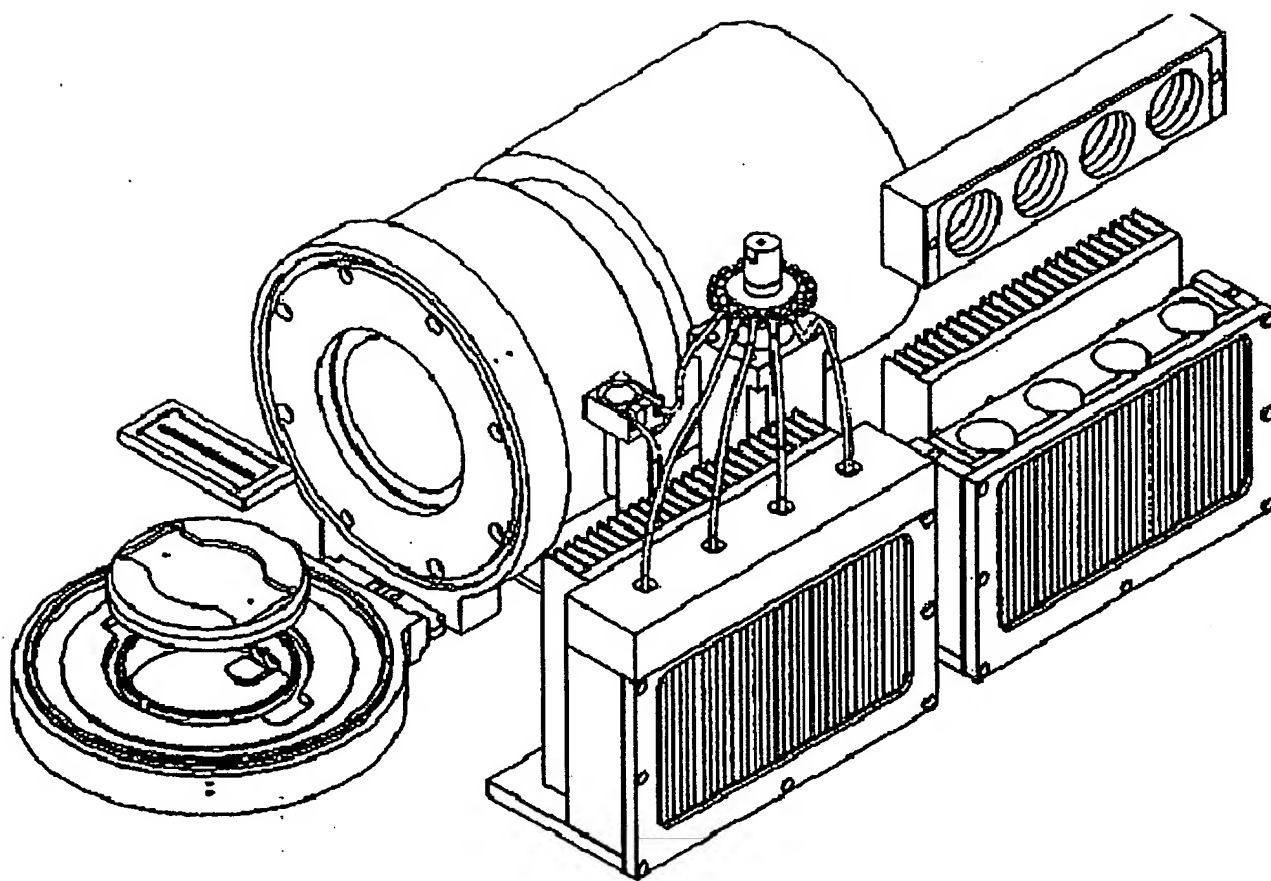


Figure 17

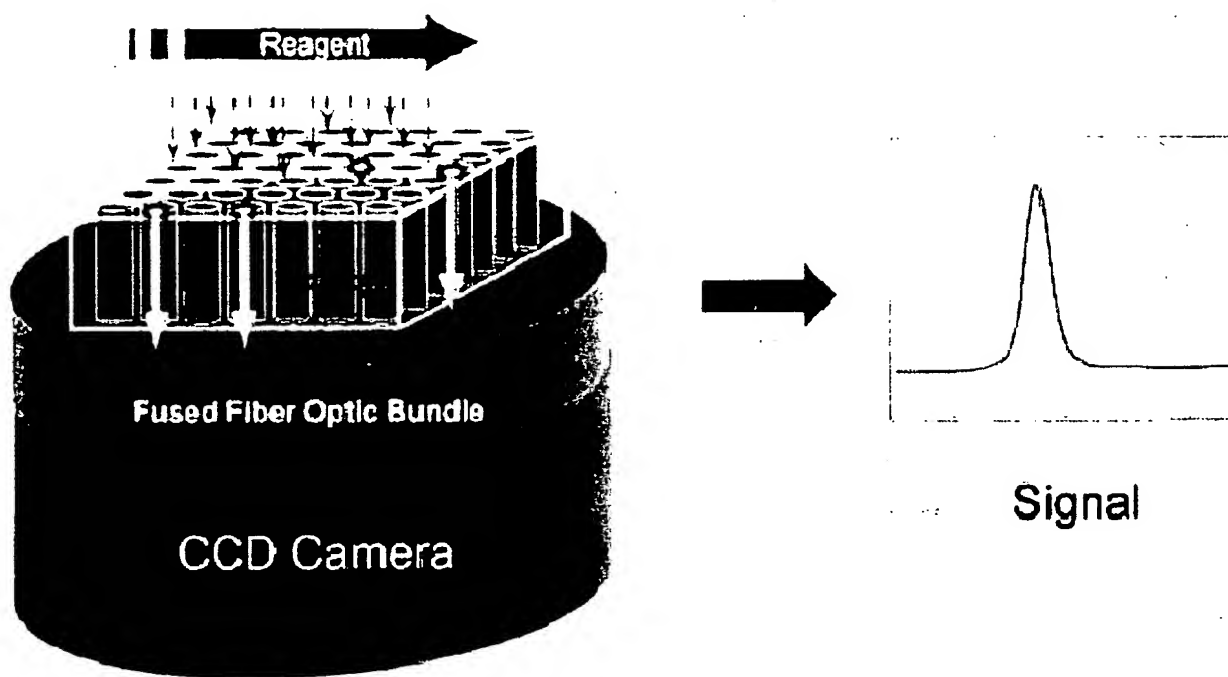
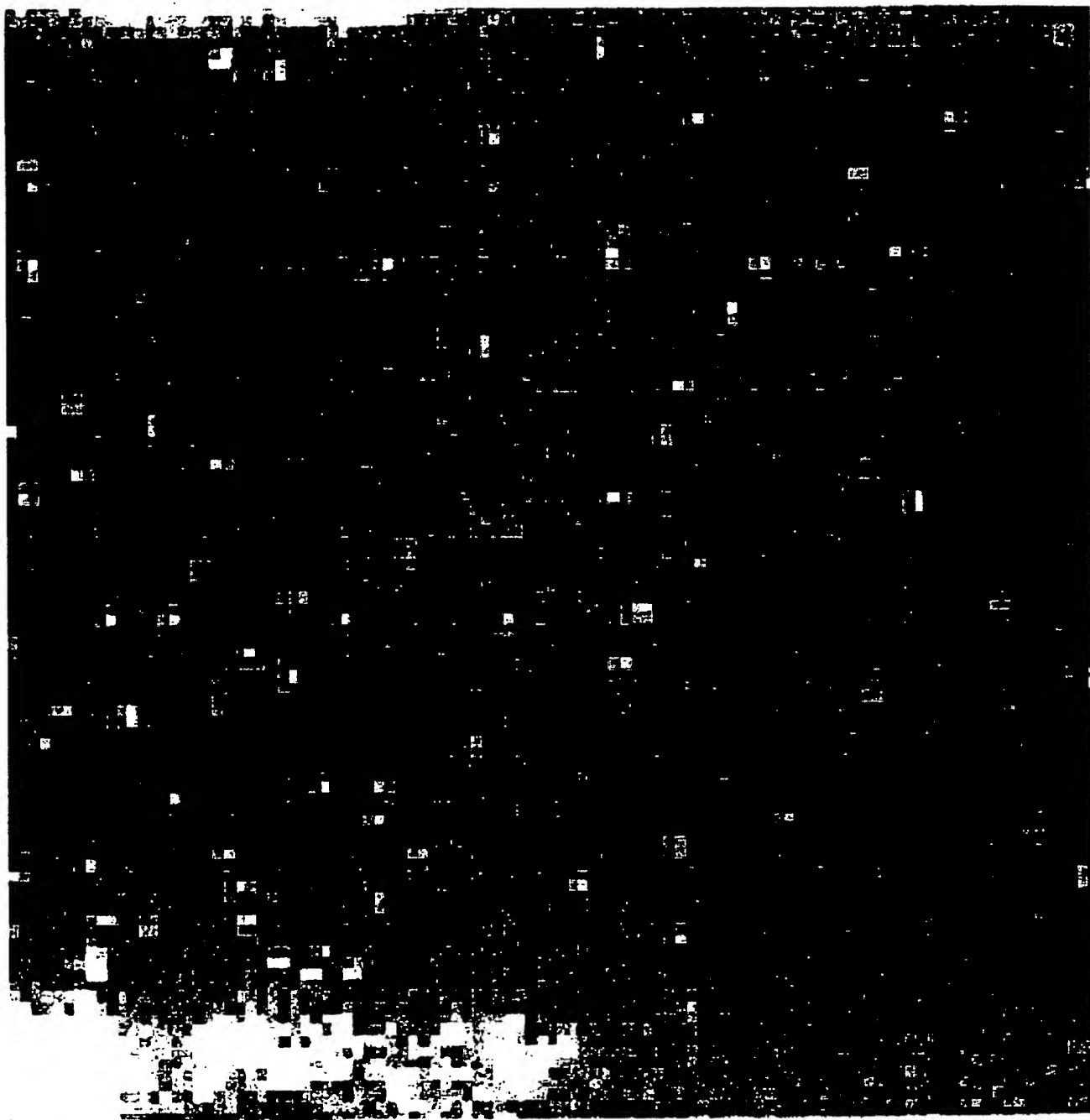


Figure 18



Sulfurylase on mobile support/Luciferase on surface, PPi flows across FORA surface. 1 mobile-support per pixel on camera; 50 $\mu$ m FORA well spanning 4 15 $\mu$ m pixels. Shown is 100 x 100 Pixels (10K pixels), 1.5 mm<sup>2</sup>.

Figure 19

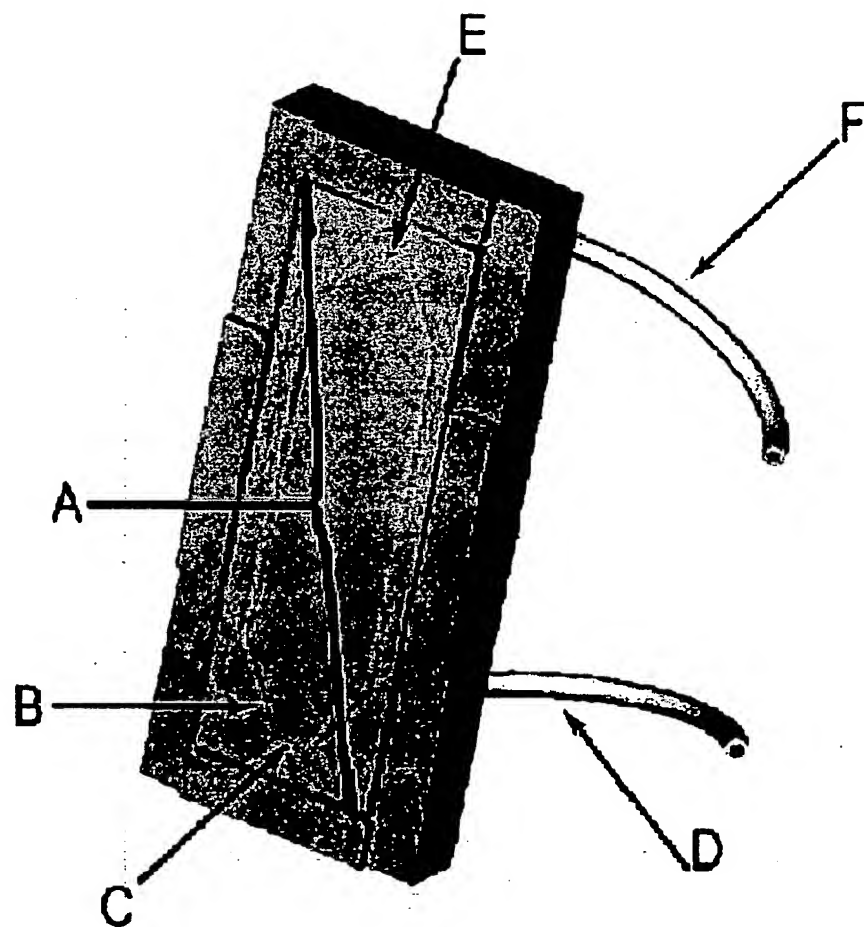


Figure 20

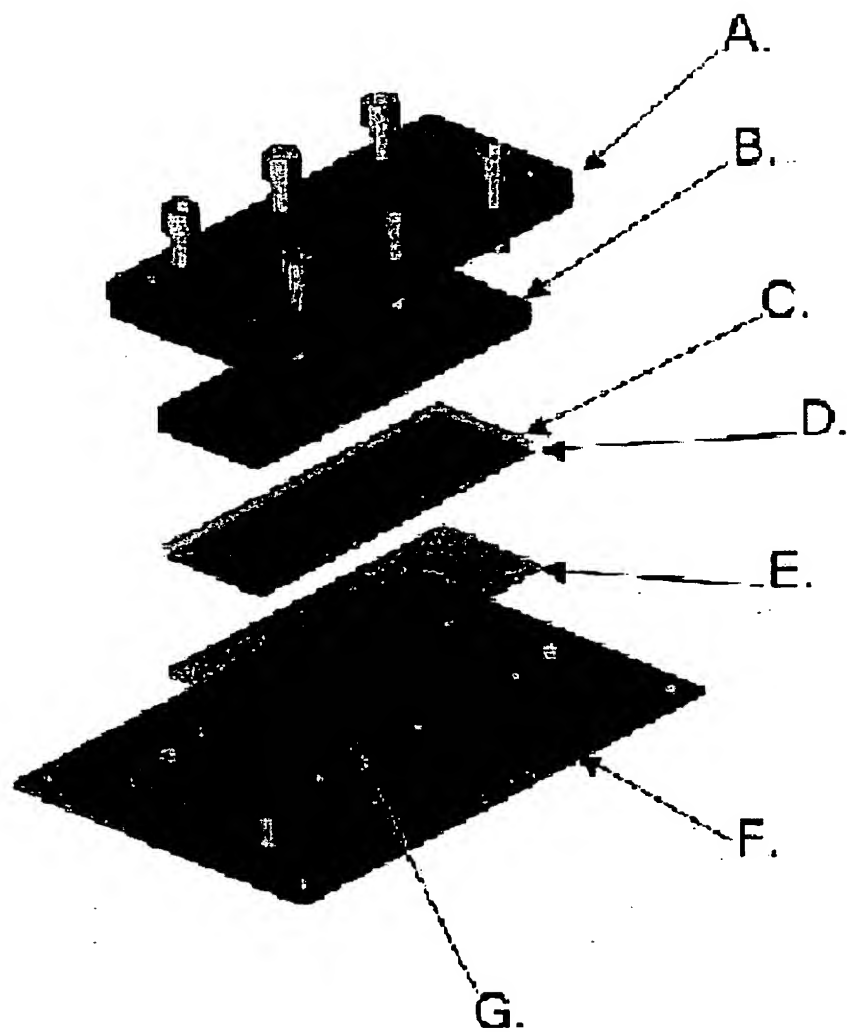


Figure 21

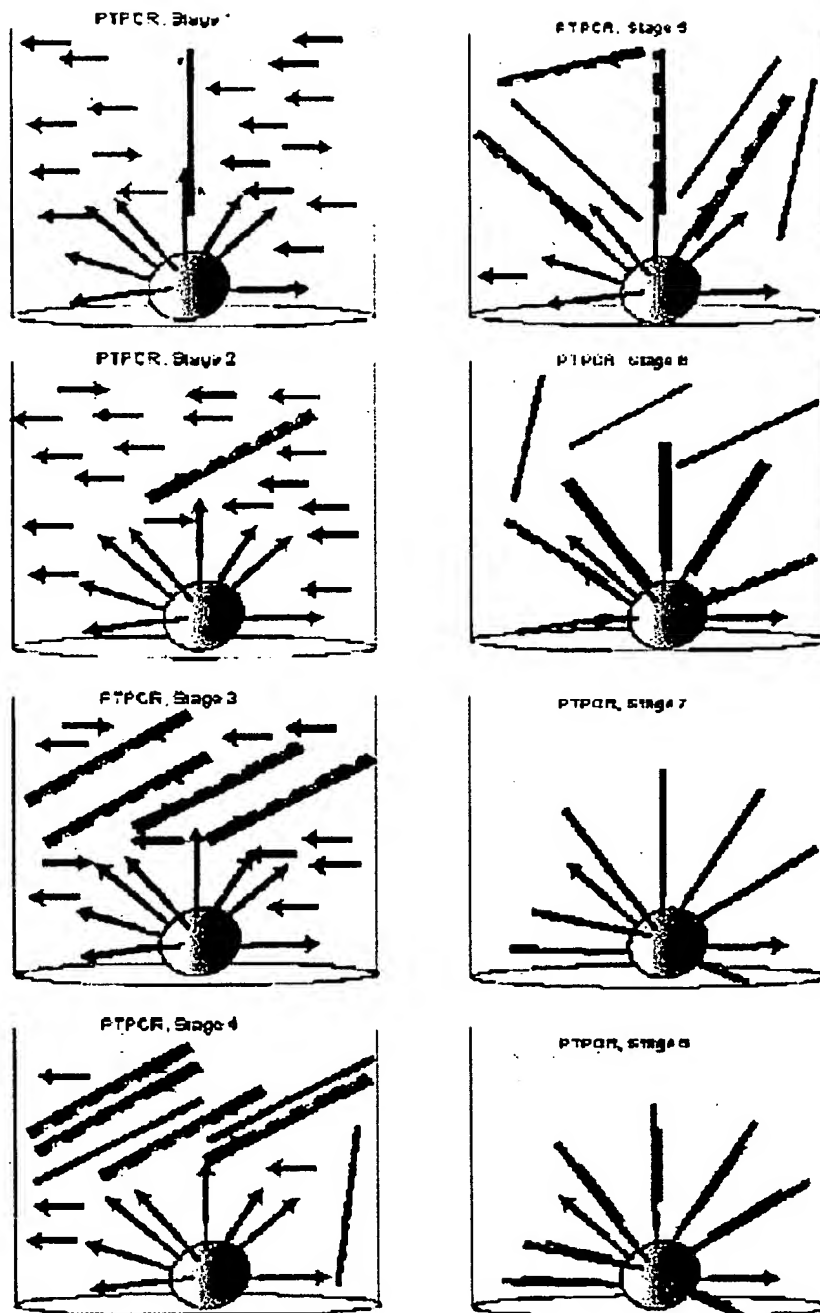


Figure 22



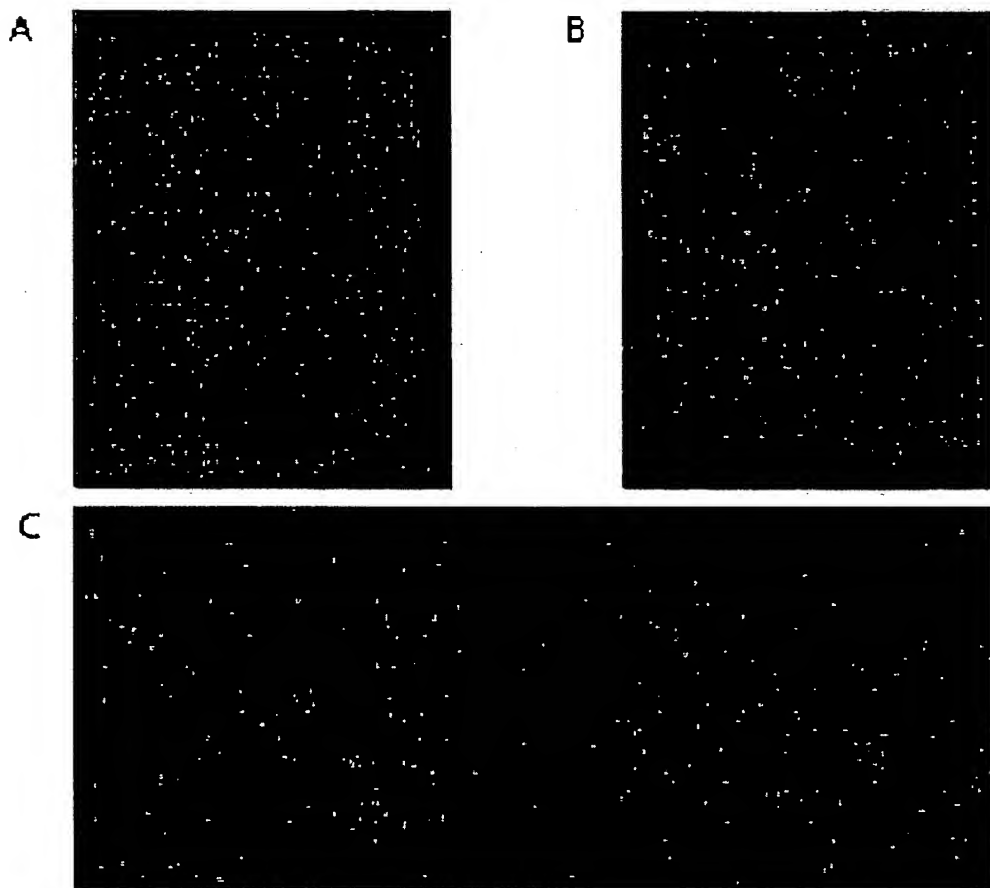


Figure 23

Figure 24

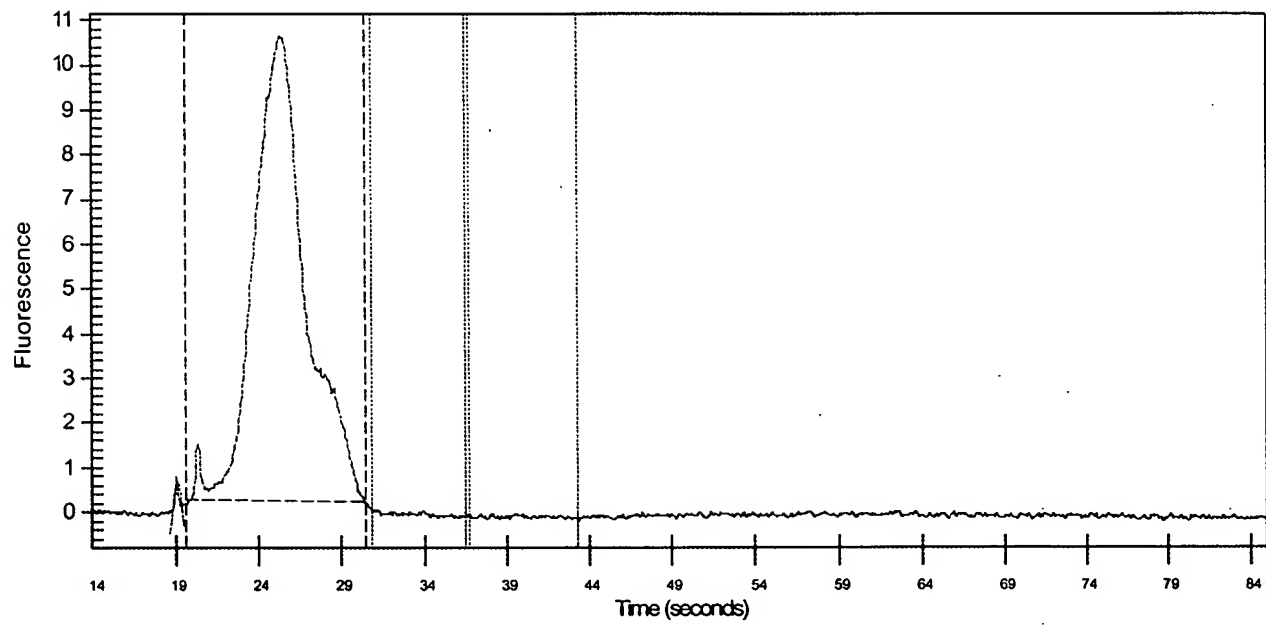


Figure ~~24~~ 25



Figure ~~26~~ 26



Figure 27

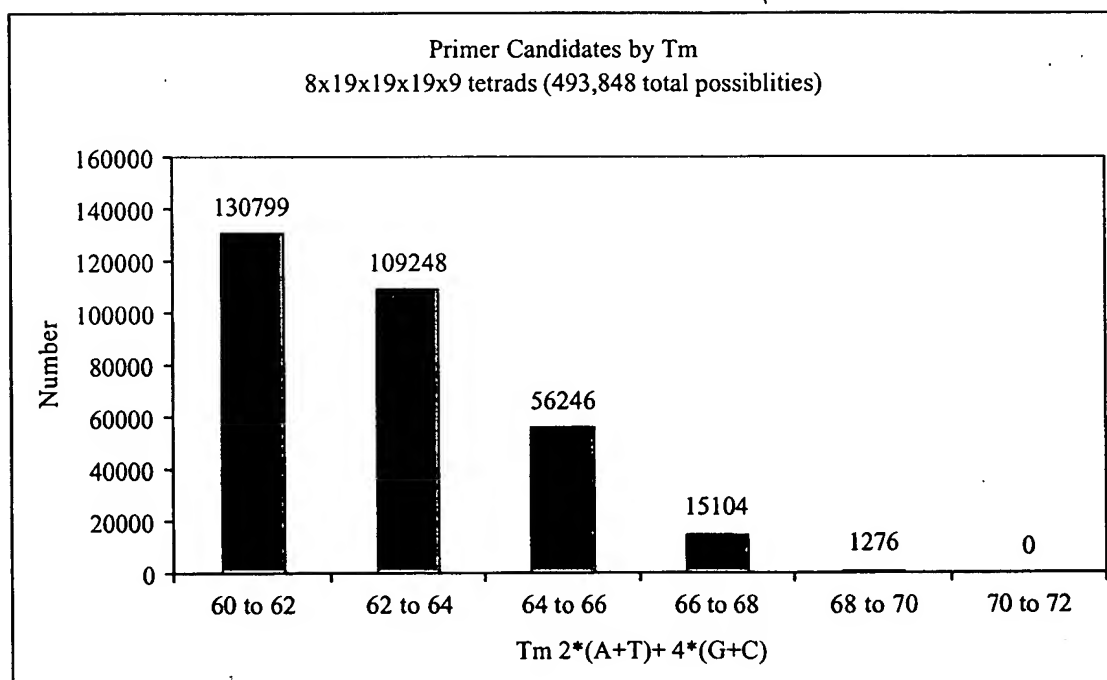


Figure 28

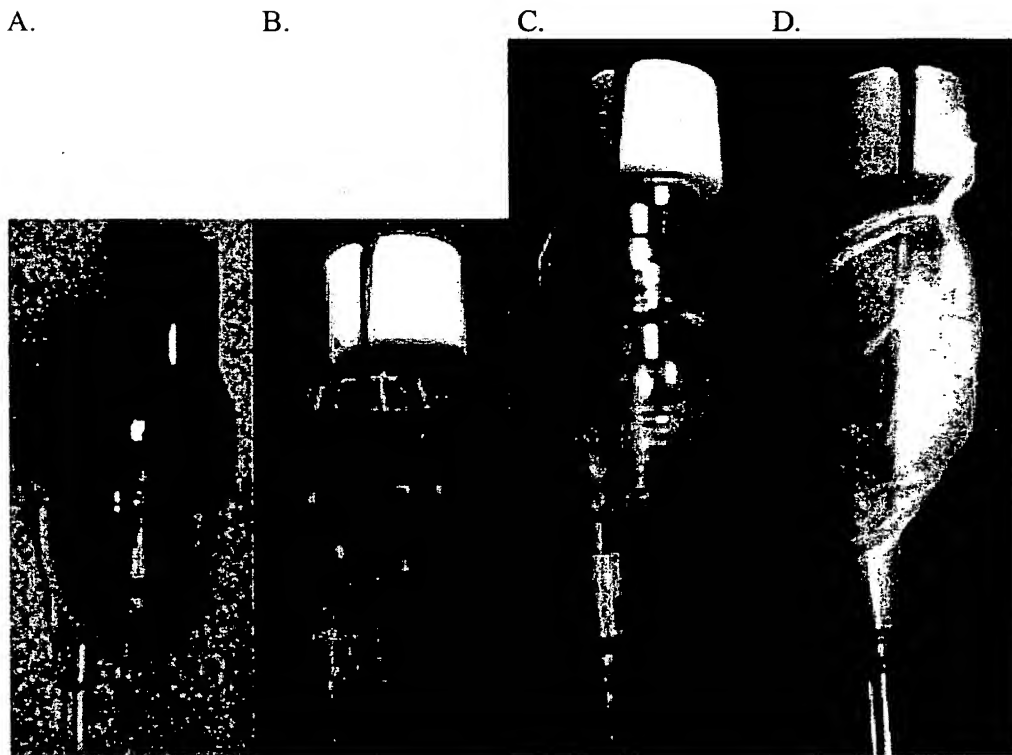


Figure 29A

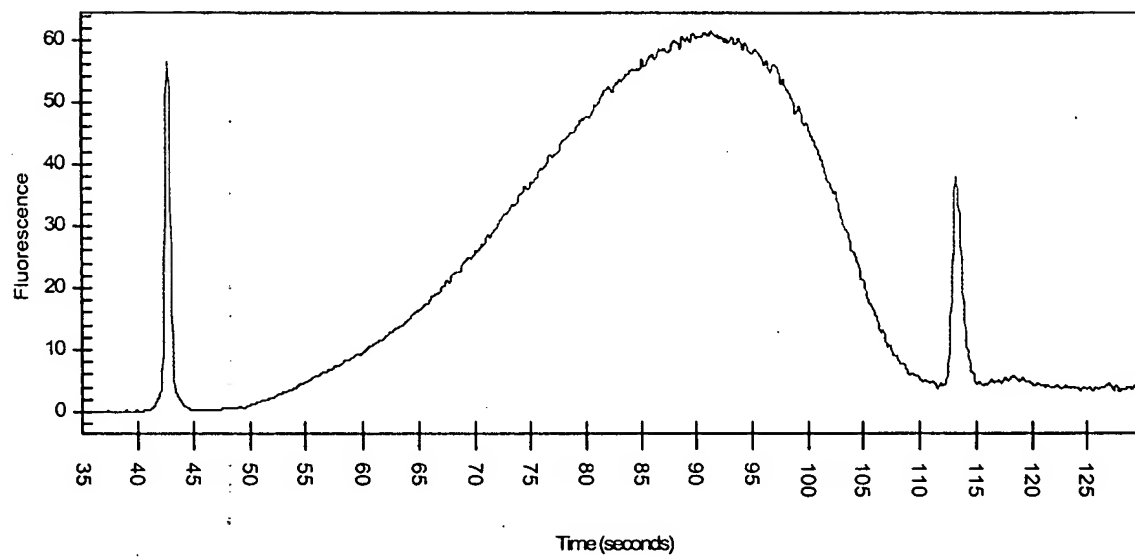
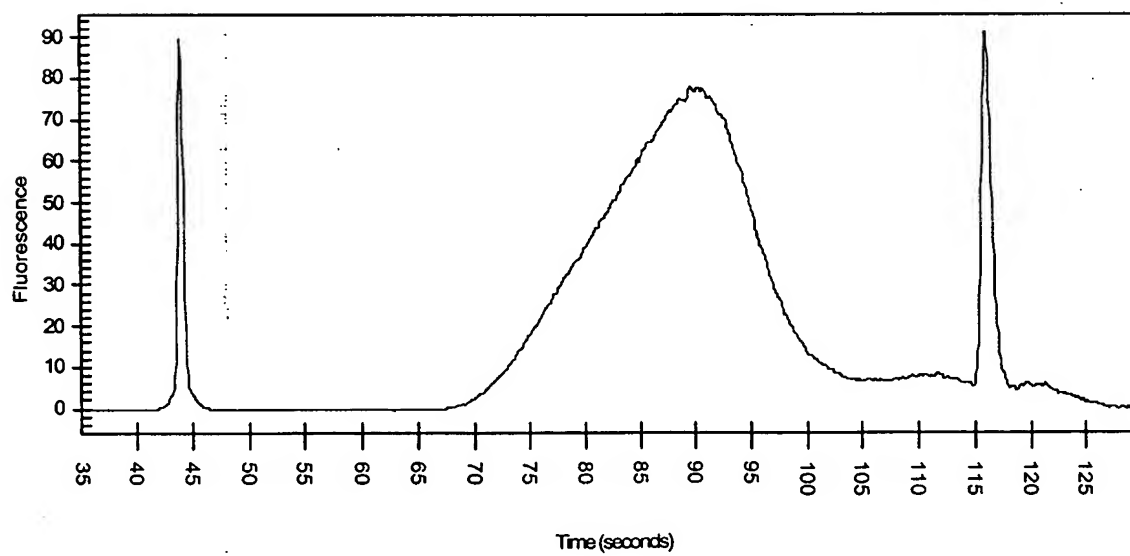


Figure 29B



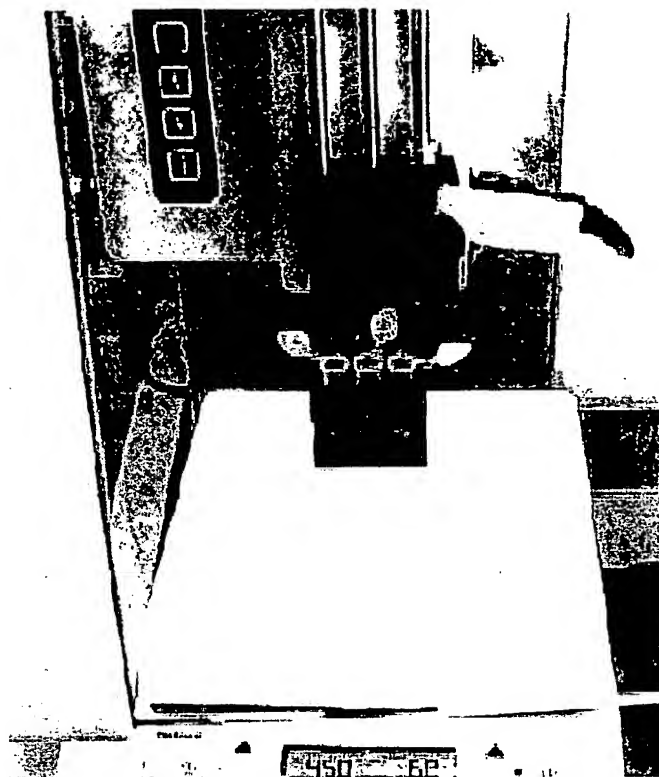


Figure 30

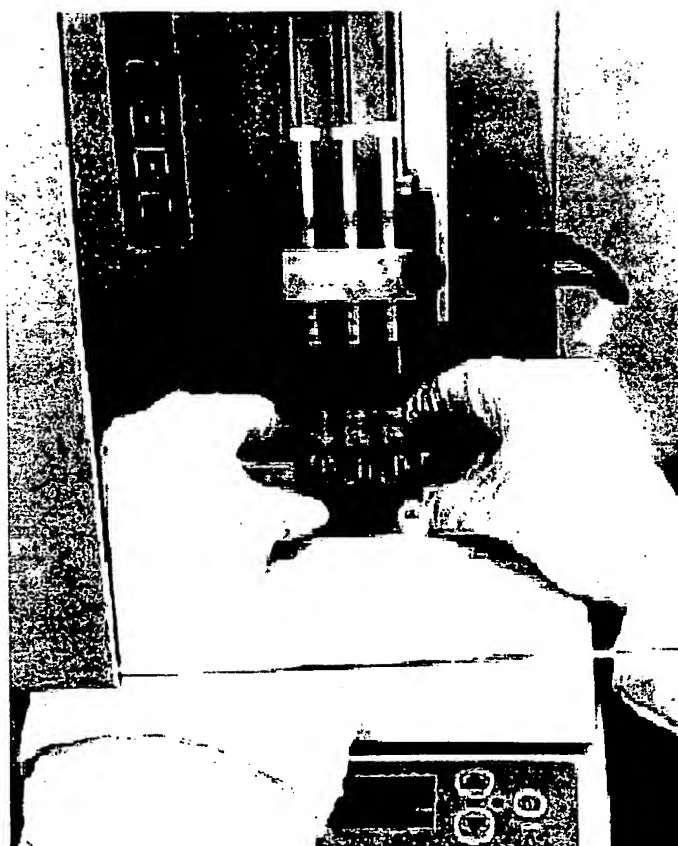


Figure 31

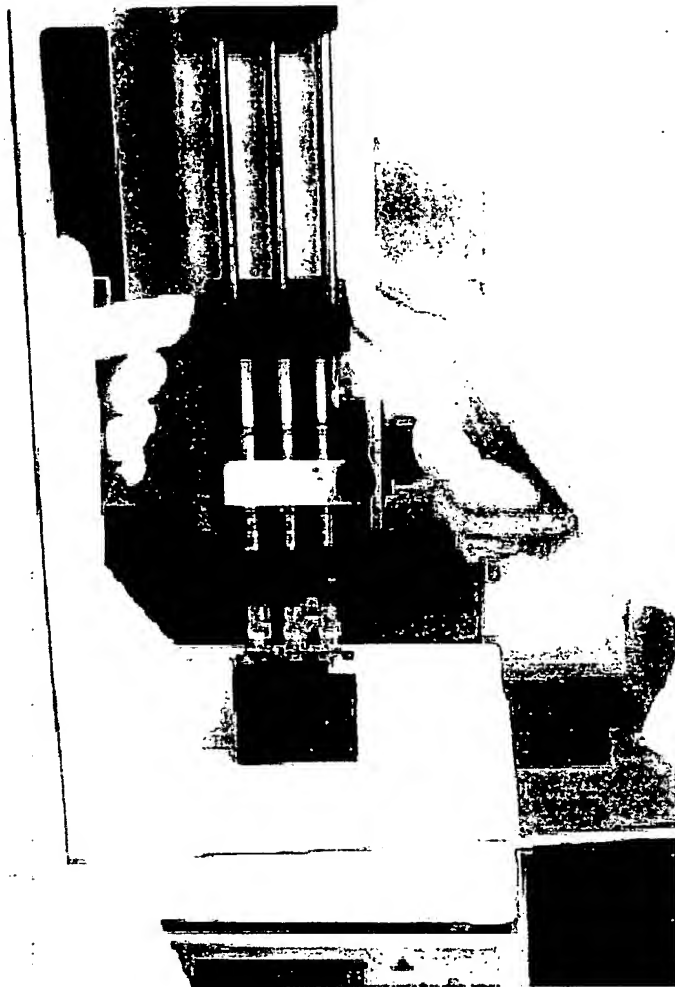


Figure 32

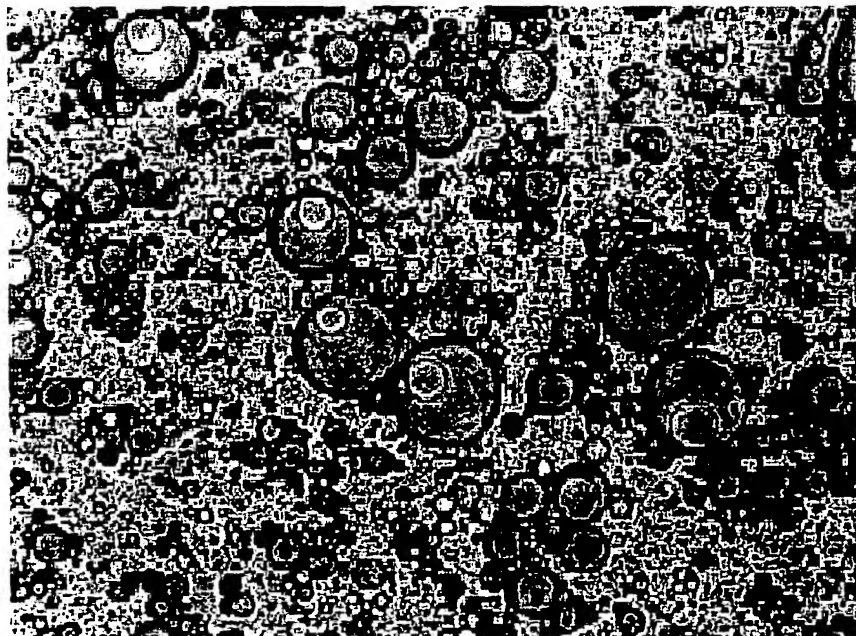
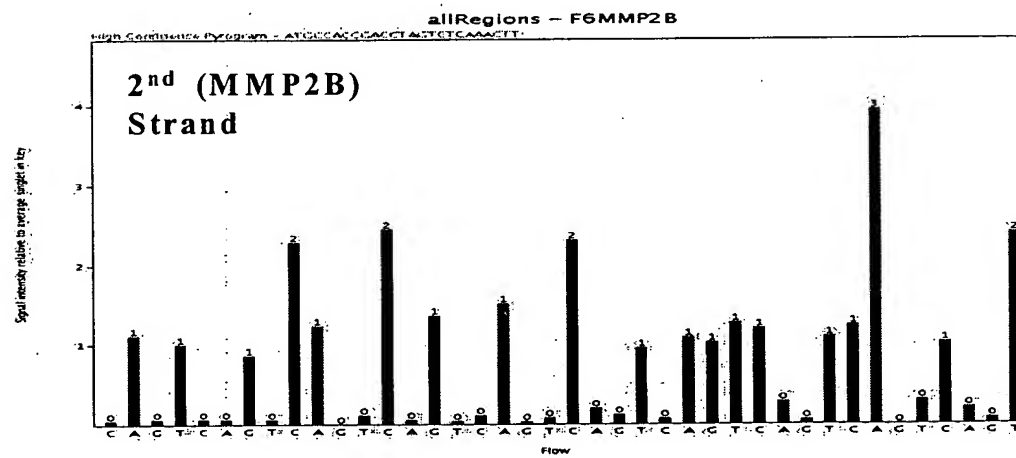
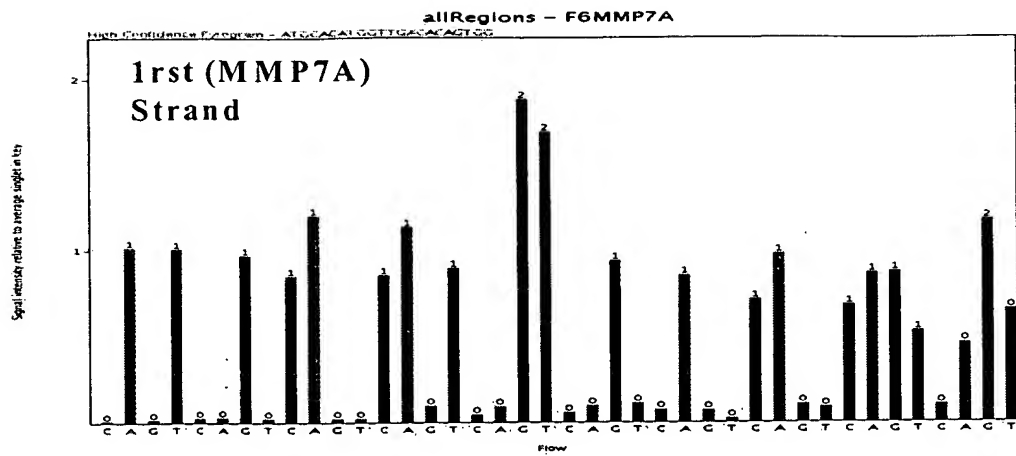


Figure 33



FIGURE 34



1st Strand  
(MMP7A)

Sample	Well Location	Sequence	Perfect Match Length
F6_14_1	00001_1362_1660.well	ATGCACATGGTTGACACAGTGGT	22

ATGC ACATGGTTGACACAGTGG

ATGC CACCGACCTAGTCTCAAACCTT

2nd Strand  
(MMP2B)

Sample	Well Location	Sequence	Perfect Match Length
F6_14_1	00003_1363_1660.well	ATGCCACCGACCTAGTCTCAAACCTT	25

Fig. 35

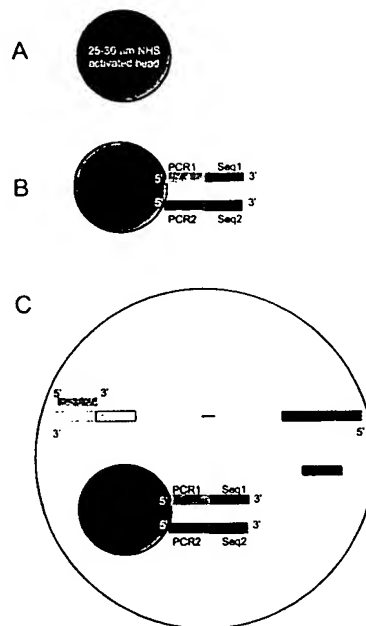


Fig. 36

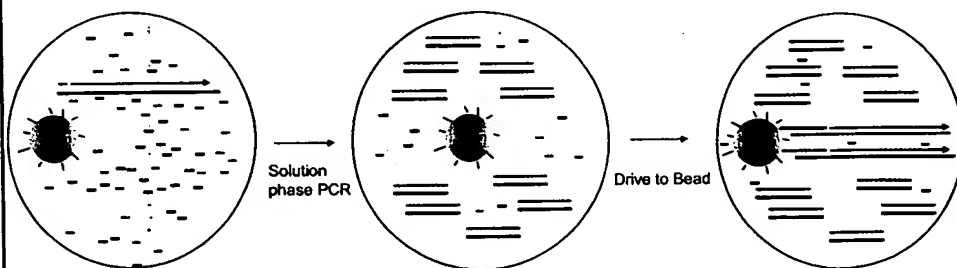


Fig.37

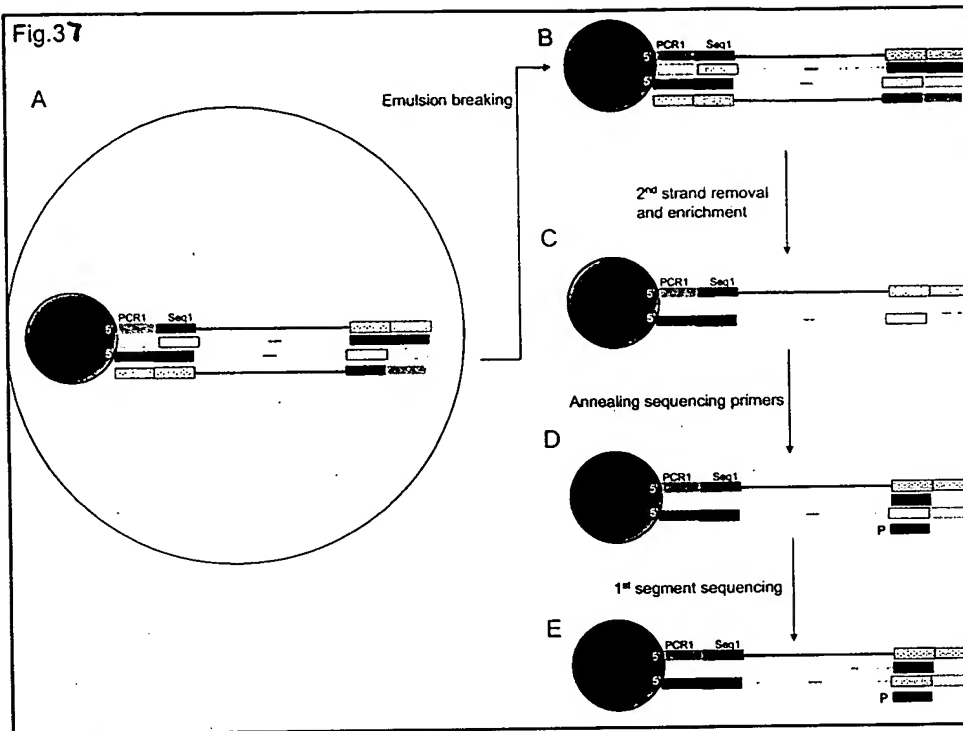


Fig. 38

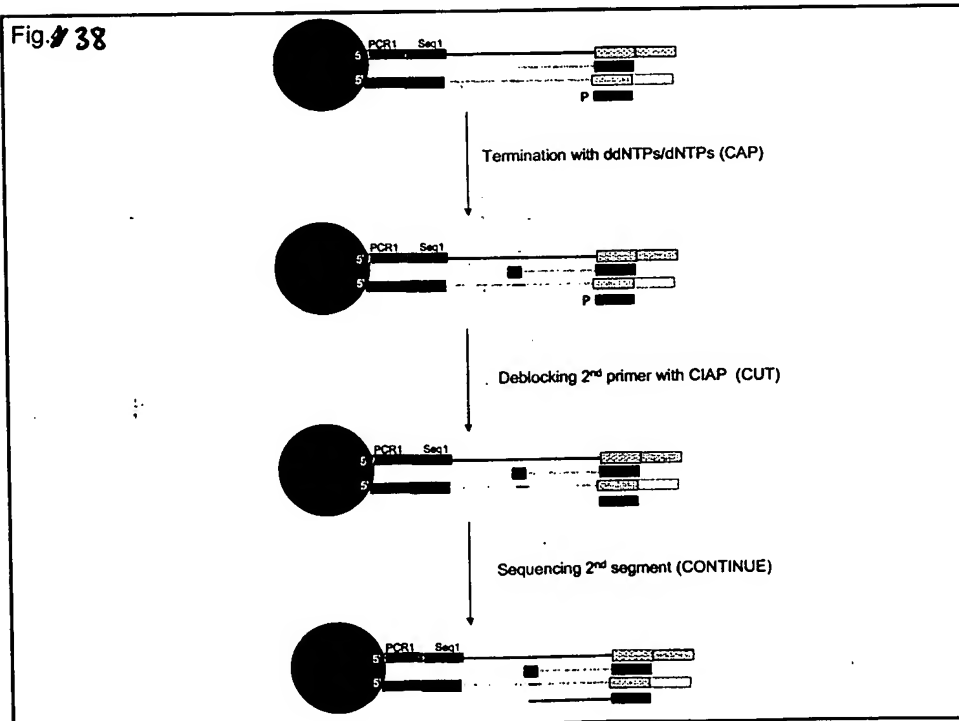
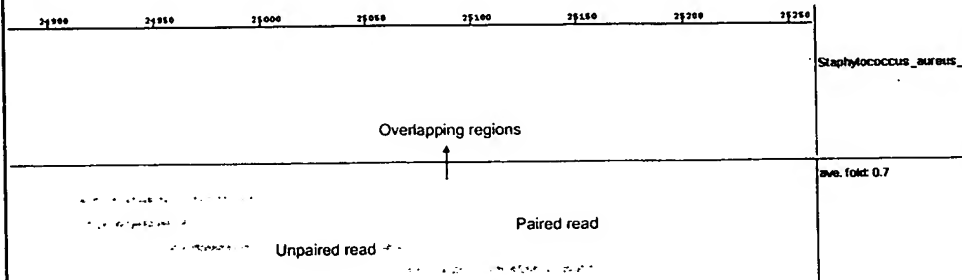


Fig. 39

A



B

Total Reads	31,785
Total 1st Strand	15,770
Total 2nd strand	16,015
Paired	11,799
Non Paired Reads	8,187
Total Coverage	38%

Fig. 40

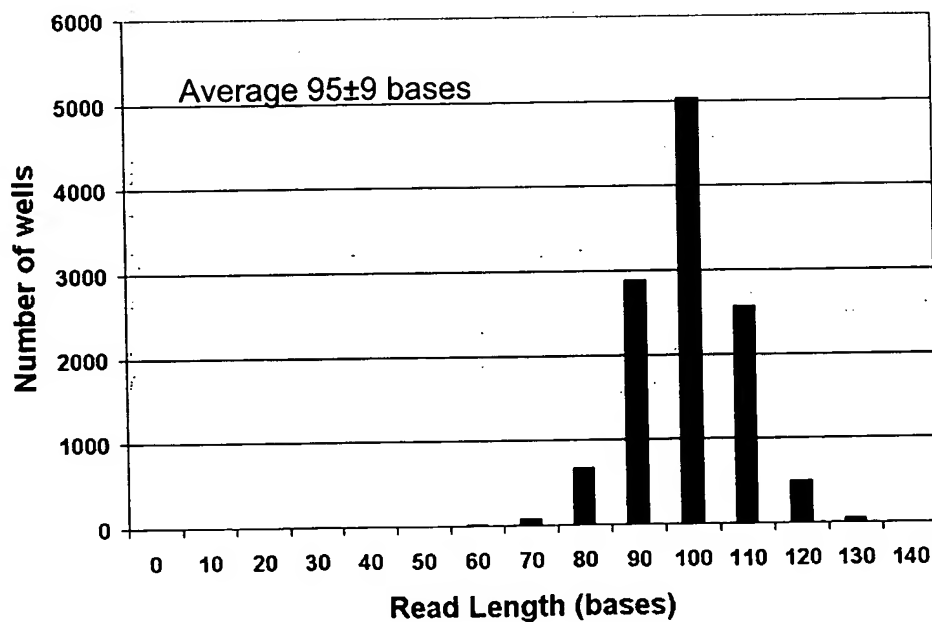


Fig. 41

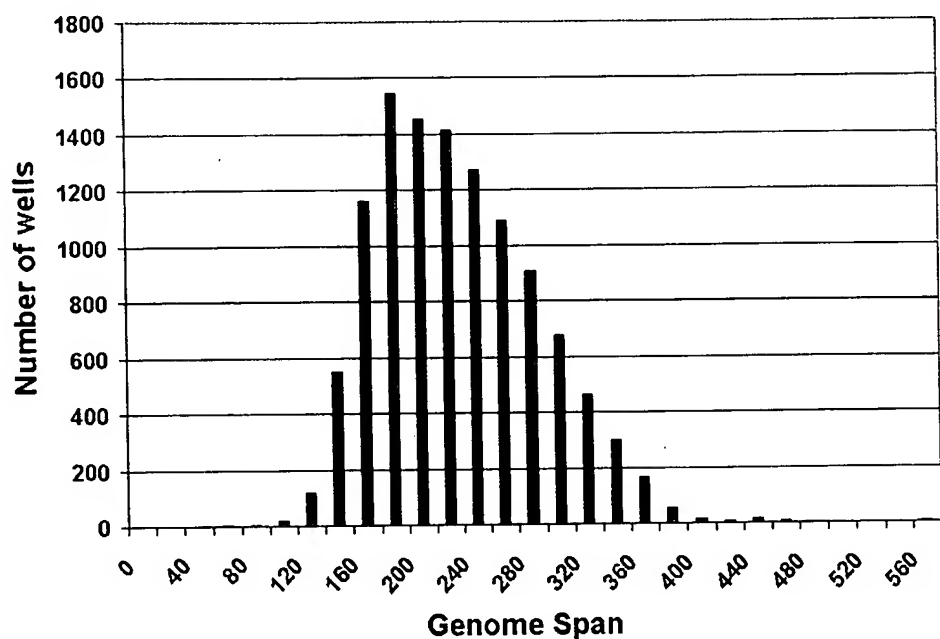


Fig. 42

Well	Genome Position	Orientation	Alignment String
00364 0548 2509	571366	F	TATTGTTGATGCTGTAAAAaGAAGCTACTGGTGTAGATTTTATGAAGTT
00364 0548 2509 D2	571512	R	TGCTCAAAGAATTCATTAAAAATGACCATAITTCATTGTATCTTT
00363 0985 2232	1487890	R	AAGCGAACAGTCAAGTACCACAGTCAGTTGACITTTACACAAGCGGAT
00363 0985 2232 D2	1487769	F	TACAGGTGTTGGTATGCCATTGCGATTGTTGCGCTTGGTTAGCCG
00397 0940 2923	2611033	F	AACATATAAACATCCCCTATCTCAATTTCCGCTTCCATGTAaCAAAAAAGC
00397 0940 2923 D2	2611164	R	TAGATATCACTTGCCTGTACTGGTAATGCAGGCATGAG
00417 0611 1933	122001	R	ATTCAACTCTGGAATGCITTCCTGATACGCCCTCGATGATG
00417 0611 1933 D2	121930	F	GATGAGGAGCTGCAATGGCAATGGGTTAAAGGCATCATCG
00434 0595 0993	2022591	R	TGTATCTCGATTGGATTAGTTGCTTTTGCATCTTCATTAGACC
00434 0595 0993 D2	2022473	F	CATTAACATCTGCACCAGAAATAGCTTCTAATACGATTGC
00443 1003 0754	107373	F	GCGACGACGTCCAGCTAATAACGCTGCACCTAAGGCTAATGATAAT
00443 1003 0754 D2	107502	R	AAACCATGCAGATGCTAACAAAGCTCAAGCAITACCAGAAACT
00454 1257 3047	59038	R	TGTTGCTGCATCATAATTAACTACATCATTTAAITCTTTGG
00454 1257 3047 D2	58880	F	GCAGATGGTGTGACTAACCAAGTTGGTCAAAATGCCCTAAATACAAAAGAT

Figure 15

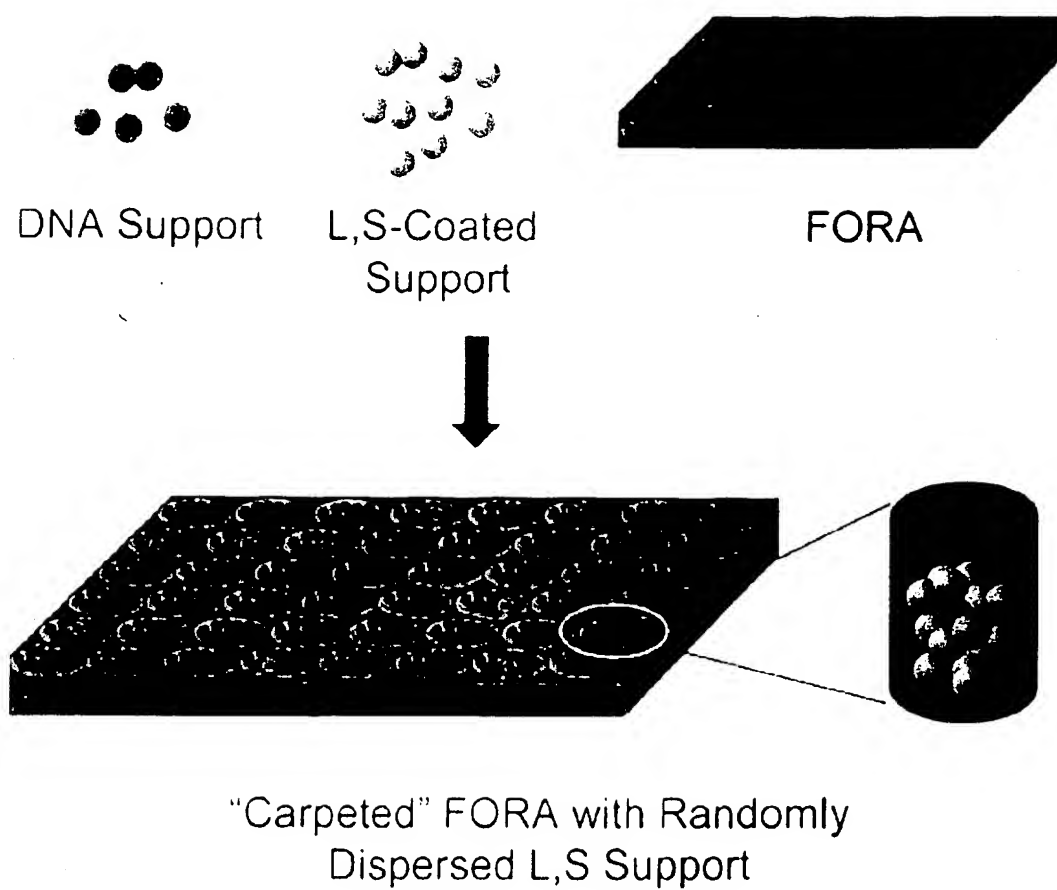


Figure 14

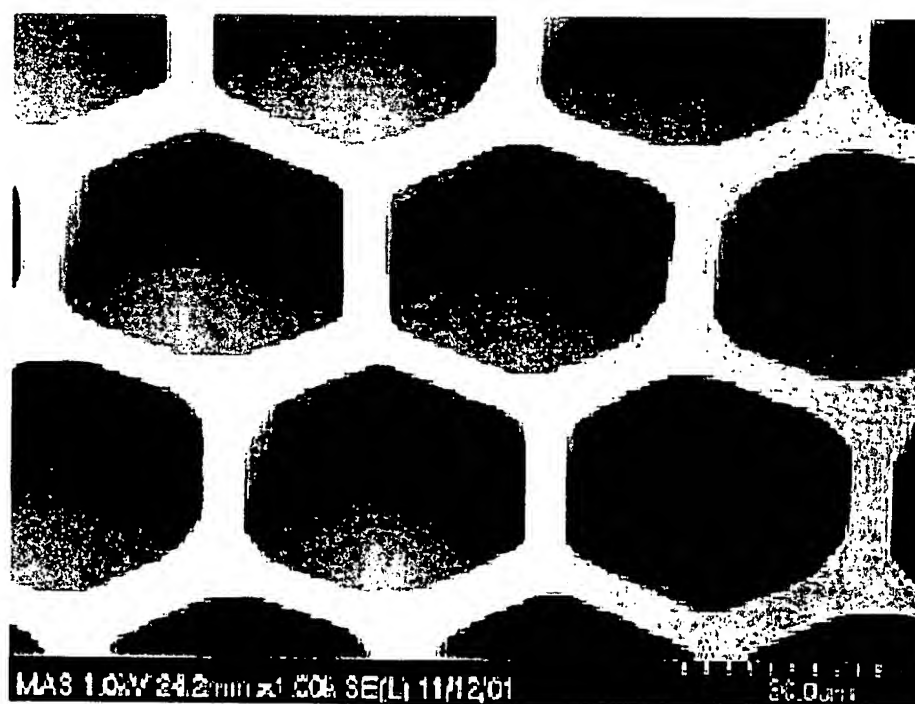
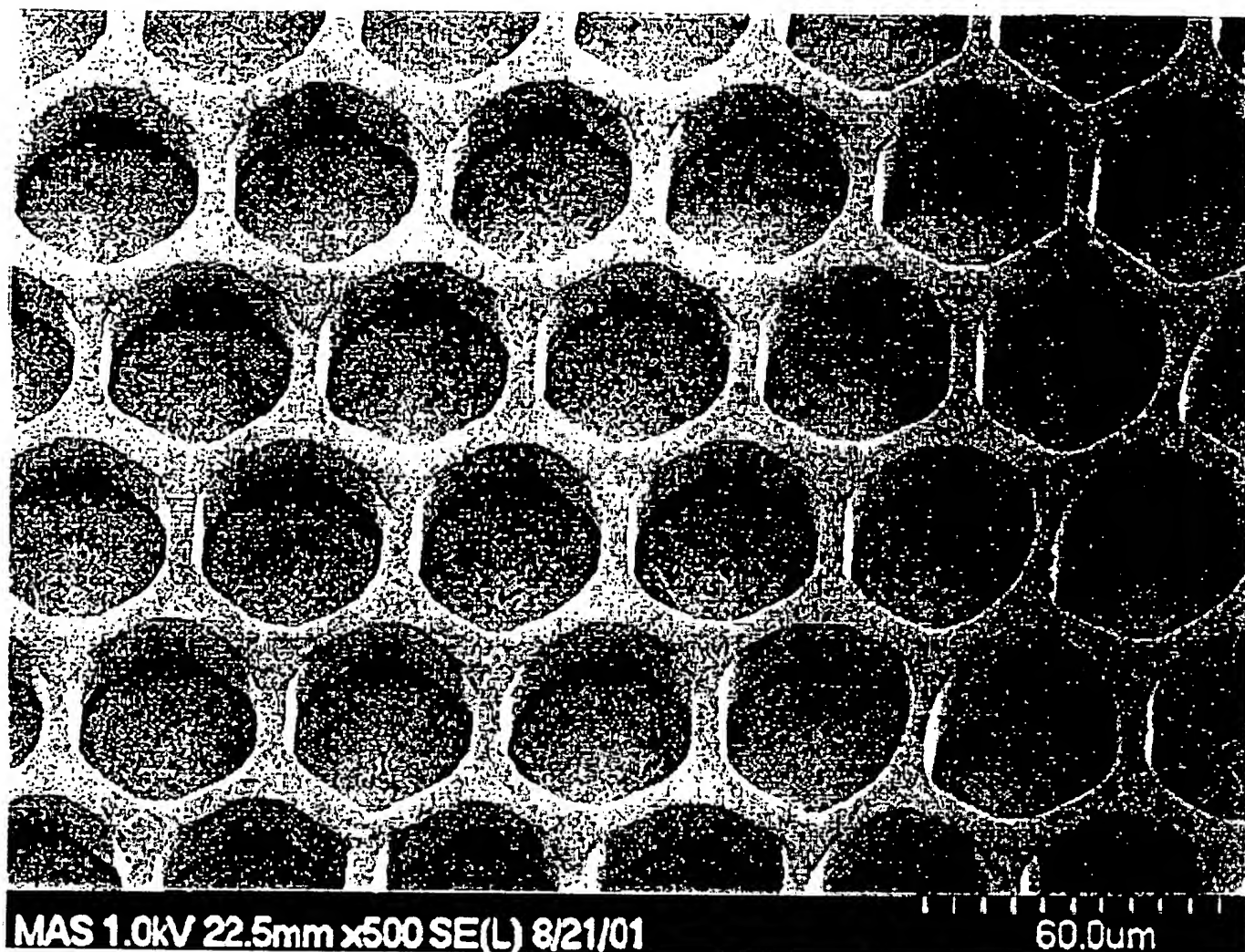


Figure 13

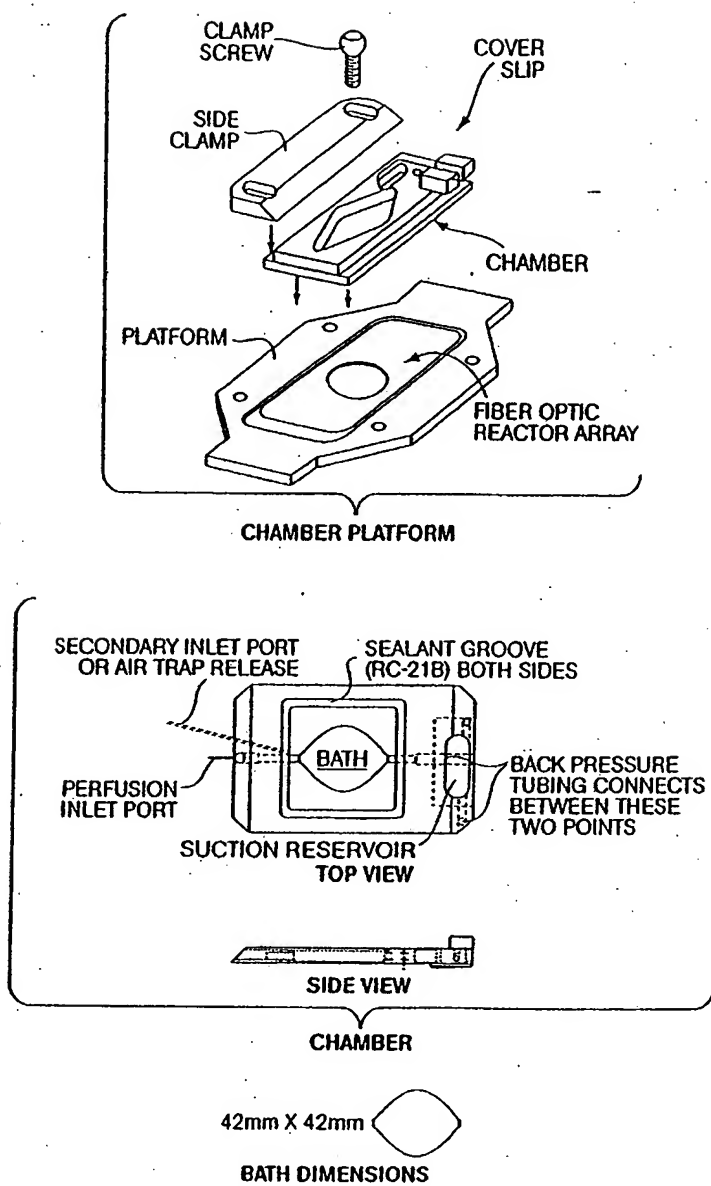


Fig. 3



Figure 12

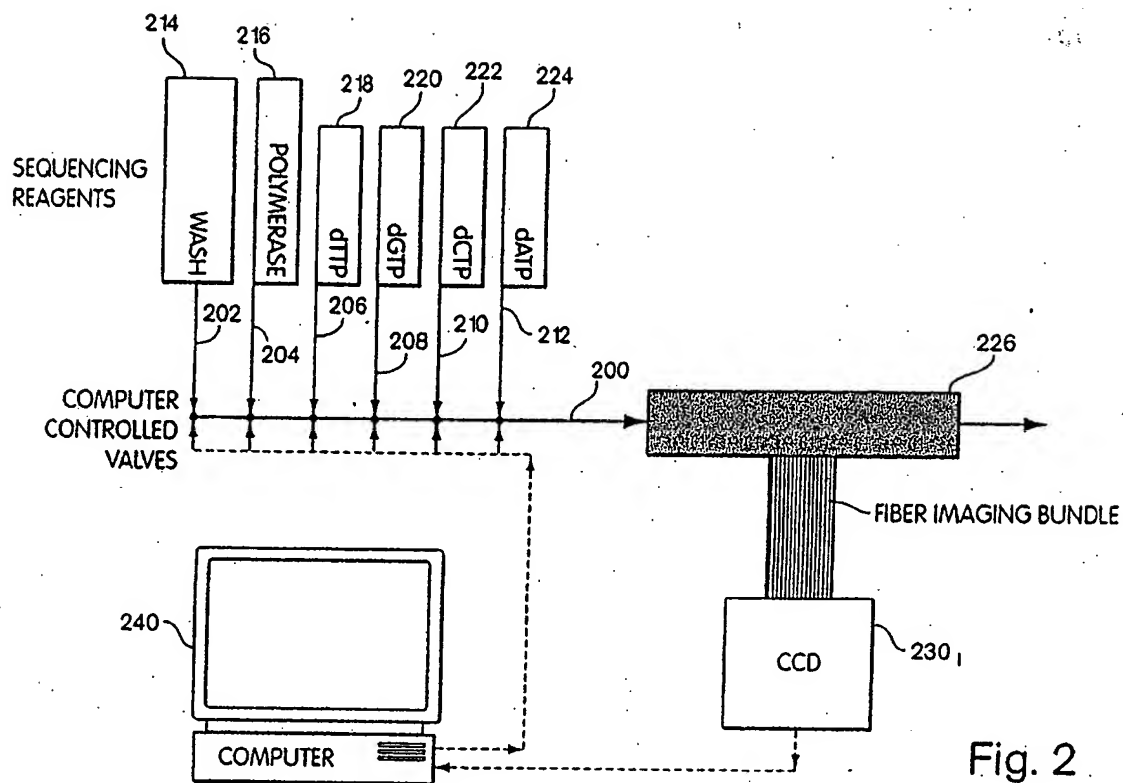


Fig. 2

Figure 11A

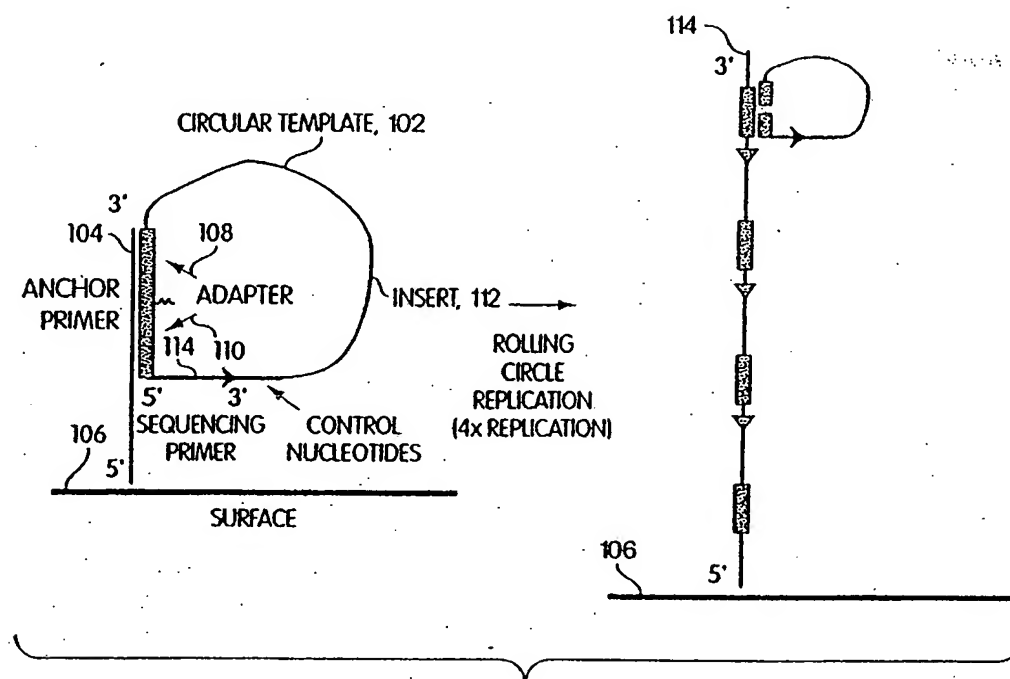


Figure 11B

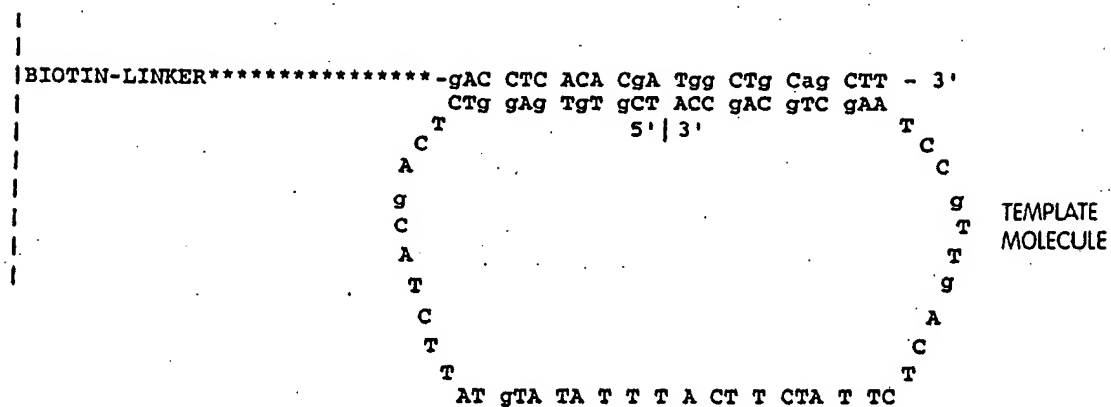


Fig. 1B

5' PHOSPHATE

3' HYDROXYL

5' NH<sub>2</sub>-His

REV STRAND

3' NH<sub>2</sub>-His

FWD STRAND

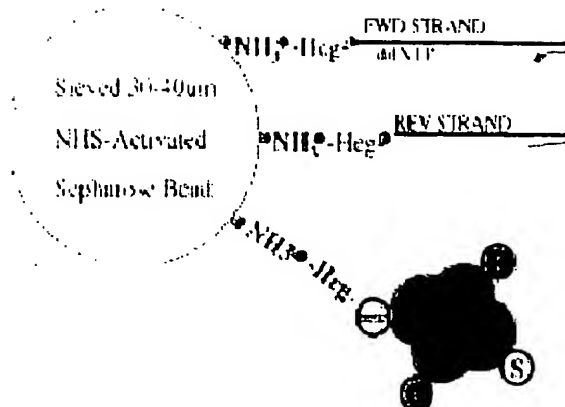
NH<sub>2</sub>-His

NH<sub>2</sub>-His

NH<sub>2</sub>-His

NH<sub>2</sub>-His

Sephacrose Bead



5' NH<sub>2</sub>-Hex

3' NH<sub>2</sub>-Hex

30-40 nm

NH<sub>2</sub>-Hex

S

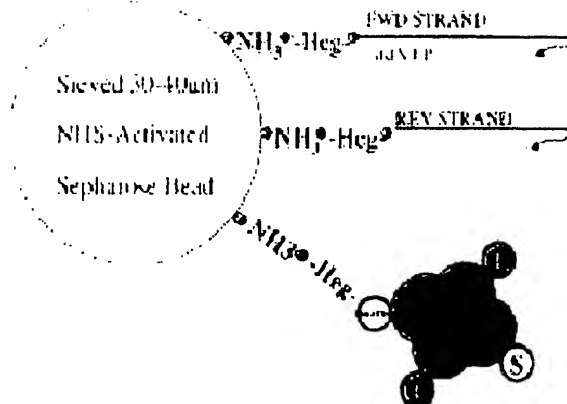


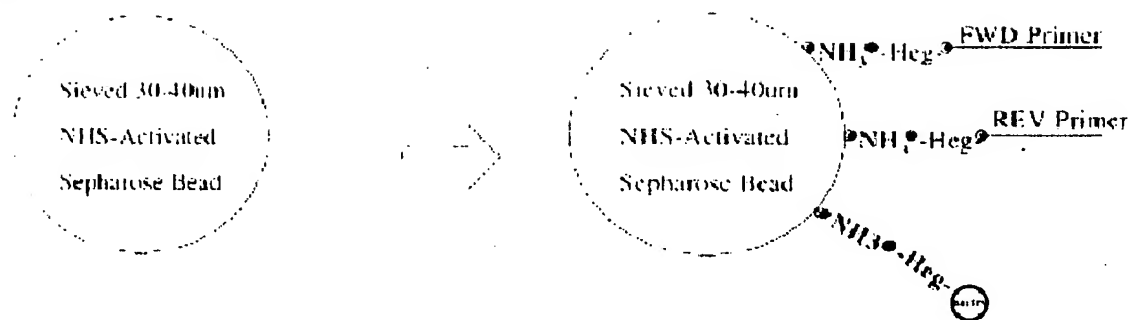
Figure 1 consists of two bar charts. The top chart is titled '1st (FWD) Strand' and the bottom chart is titled '2nd (REV) Strand'. Both charts have a y-axis labeled 'COUNT' ranging from 0 to 100 and an x-axis labeled 'LENGTH' ranging from 1 to 100. The bars represent the frequency of each length. In the top chart, the distribution is roughly bell-shaped, peaking at length 10 with a count of approximately 90. In the bottom chart, the distribution is also roughly bell-shaped, peaking at length 10 with a count of approximately 80.

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1 -ADP: ADDRESSING DATA SETS = (PAGE THREE)*****  
2 -SYNOPSIS AND OBJECTIVES = (PAGE FOUR)*****
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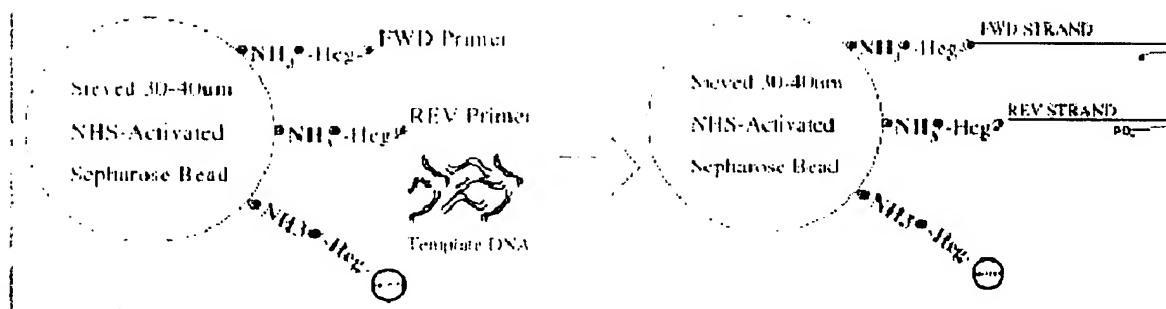
Sample	Yell (moss)	Sagebrush	Peridot Marsh/Larrea
10-14-9	UNDER THE ROCKS	ALL OVER THE PLANT	

FIGURE 10

A.)



B.)



C.)

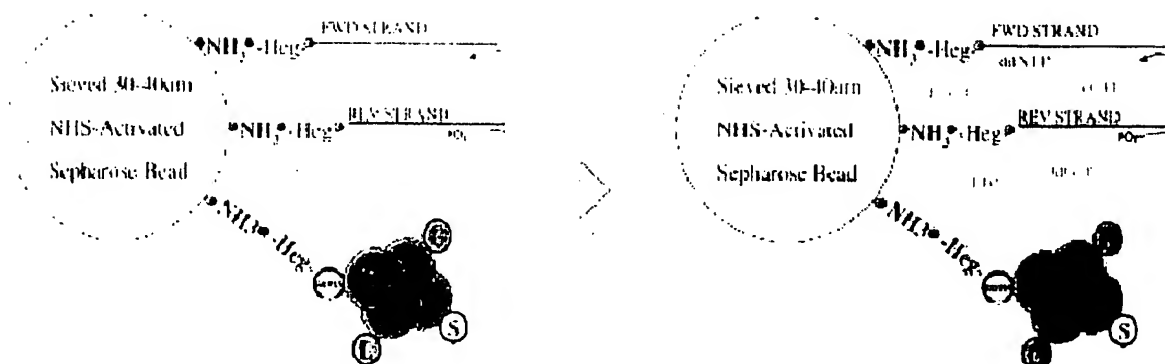
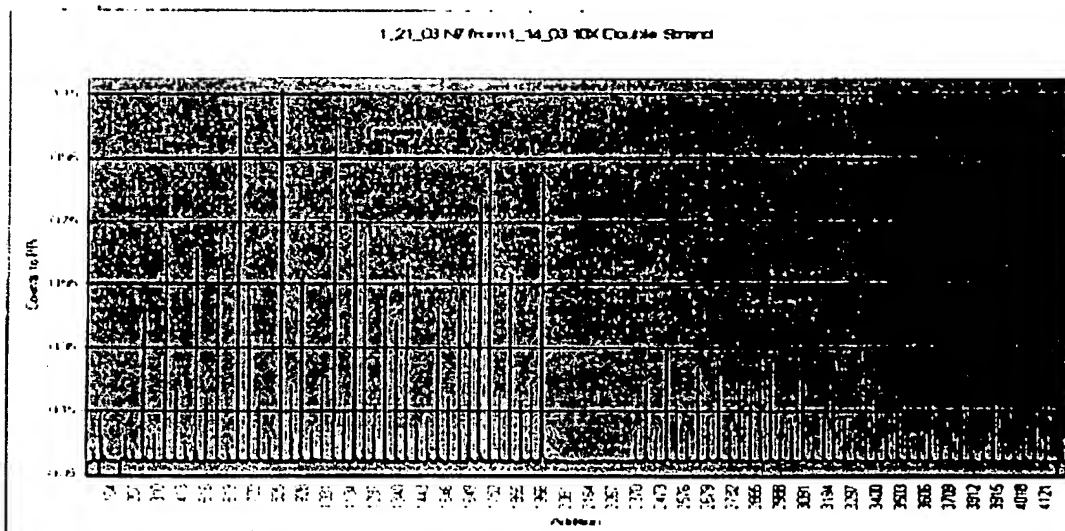


FIGURE 9



NYC 261535v2

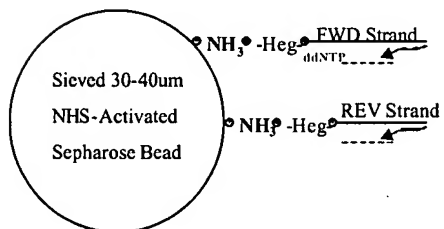
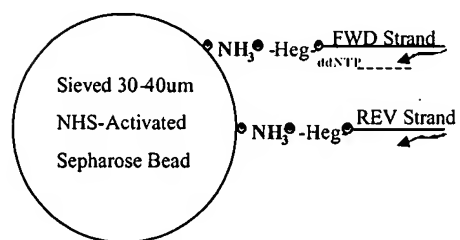
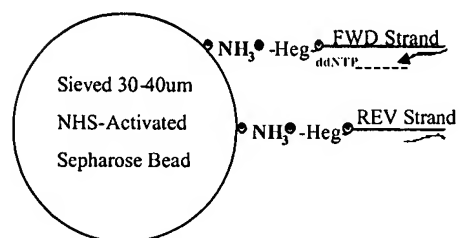
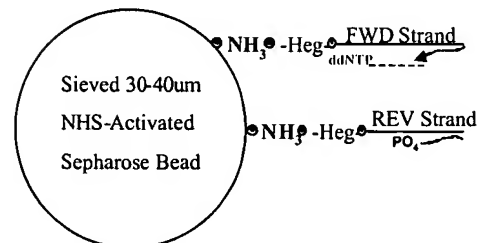
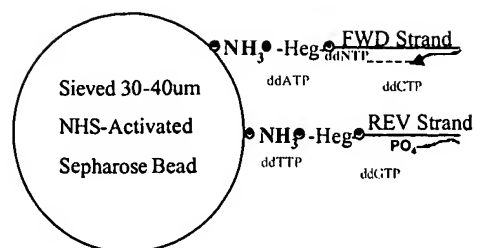


FIGURE 8

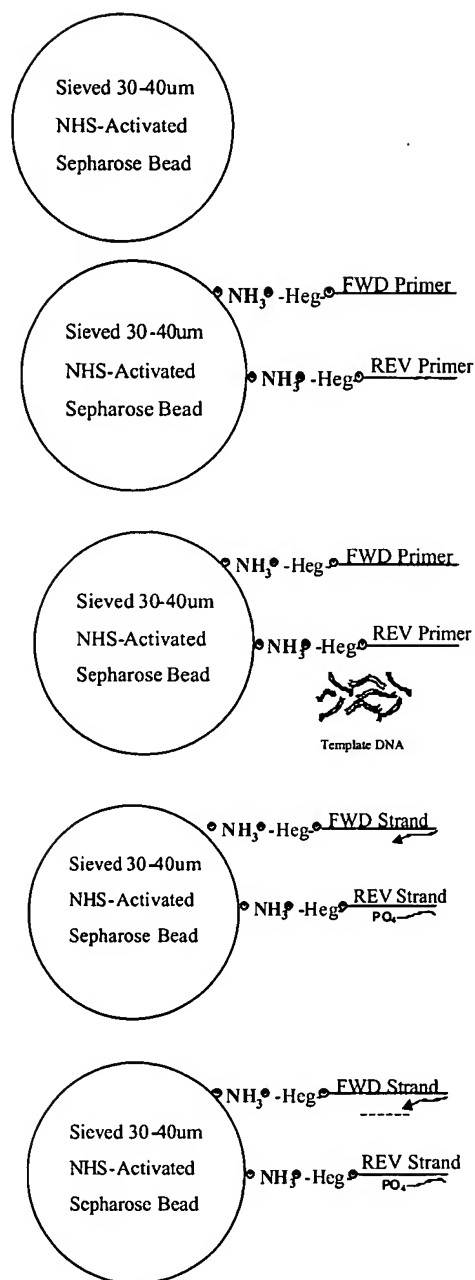


FIGURE 7

## Schematic Process Flow for Bead Separation

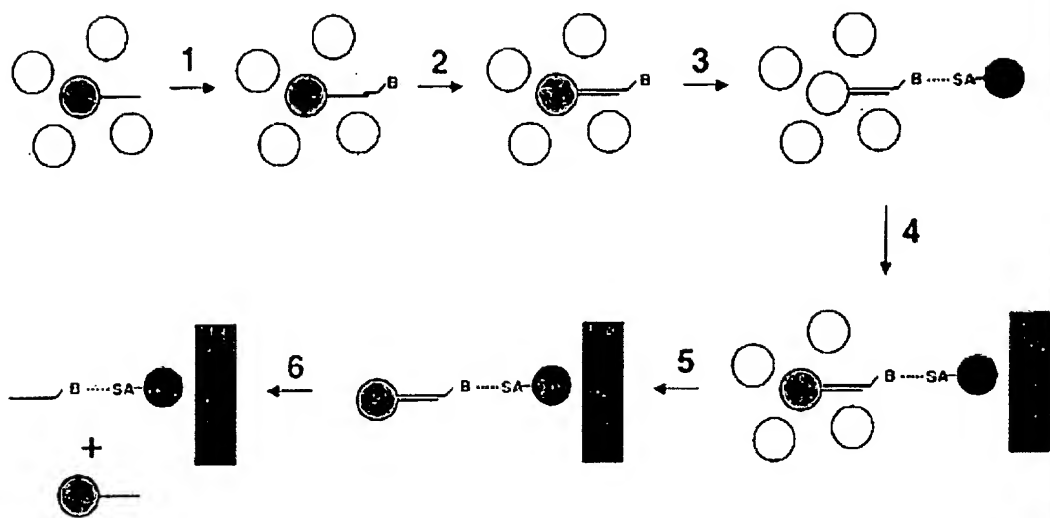




FIGURE 6B

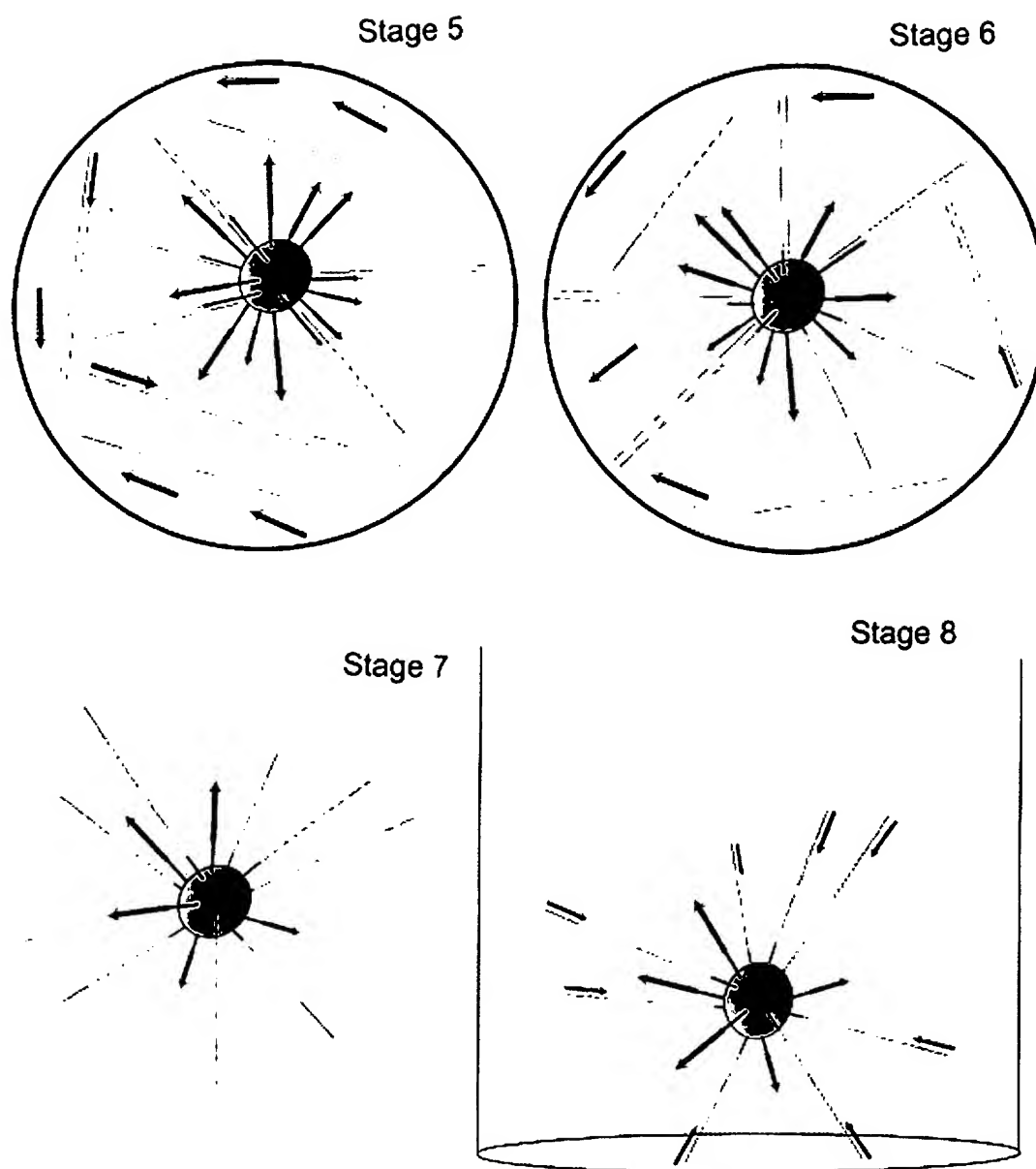


FIGURE 6A

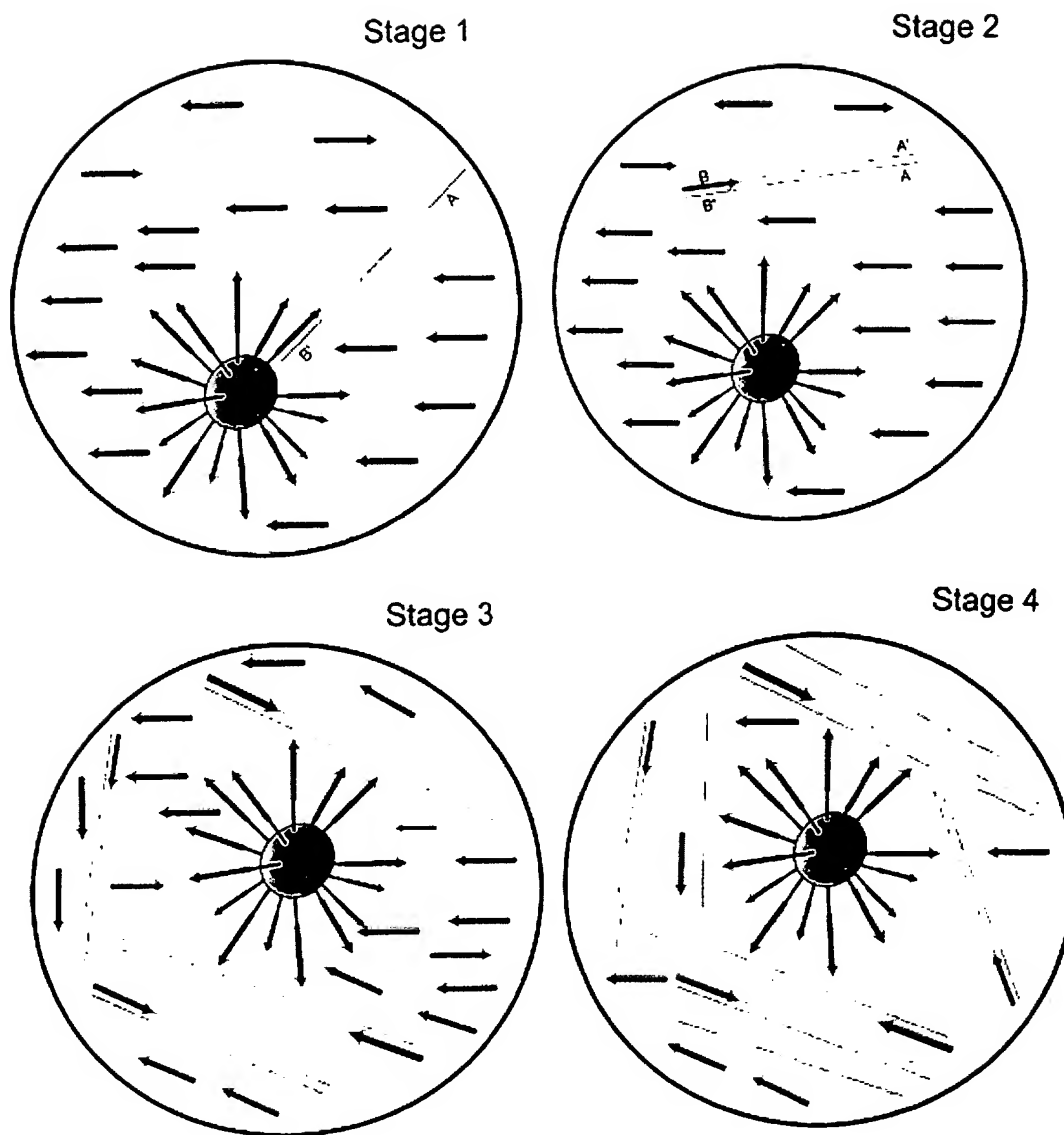


Figure 5

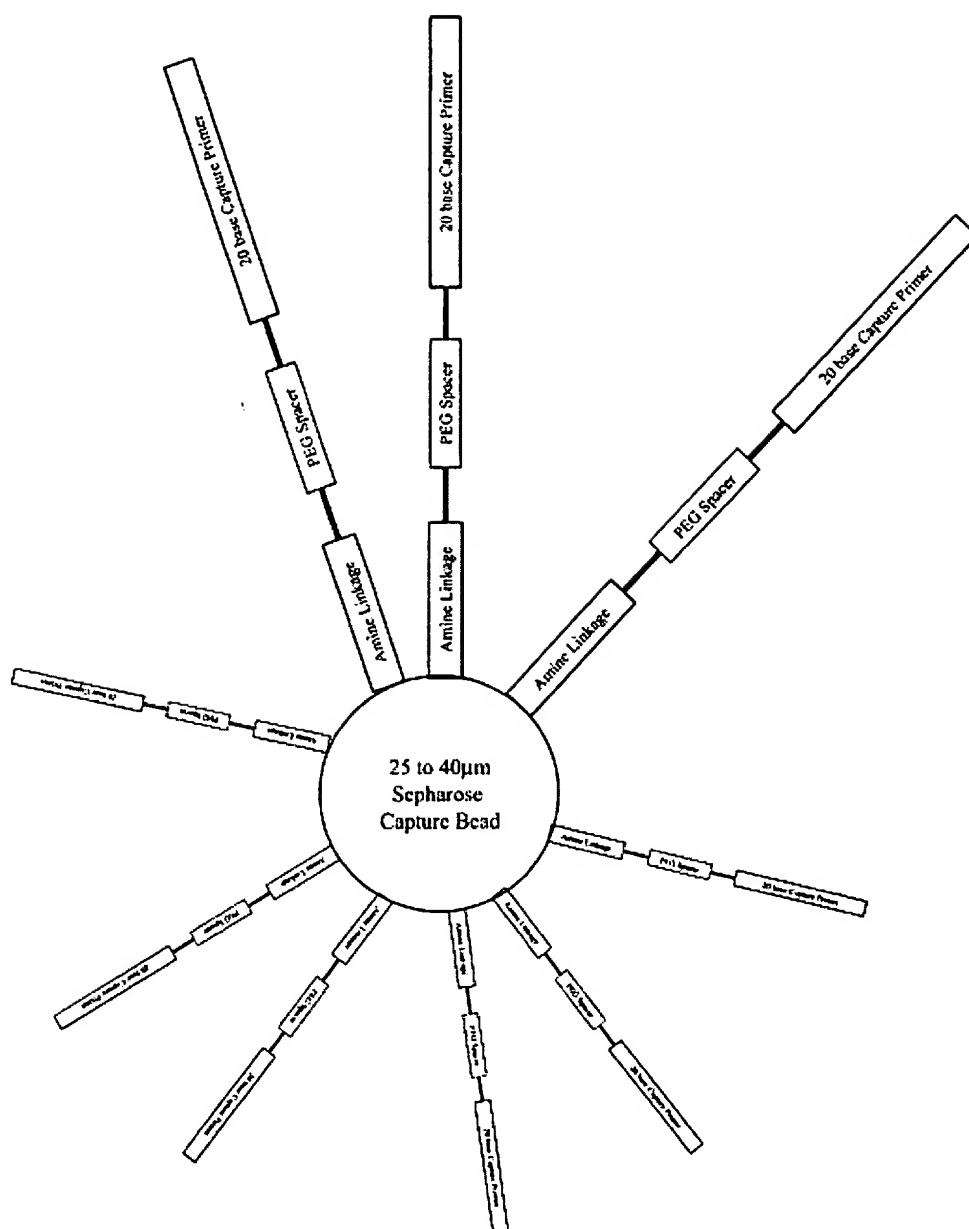


Figure 4

# Possible double-stranded Genomic DNA Library Species:

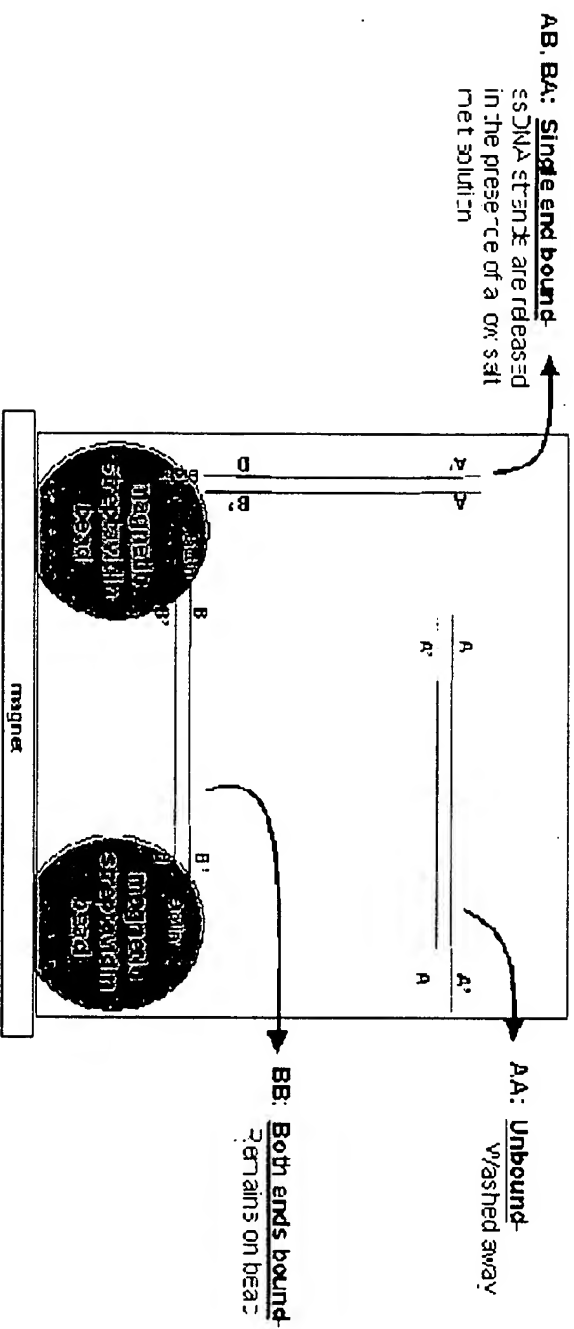
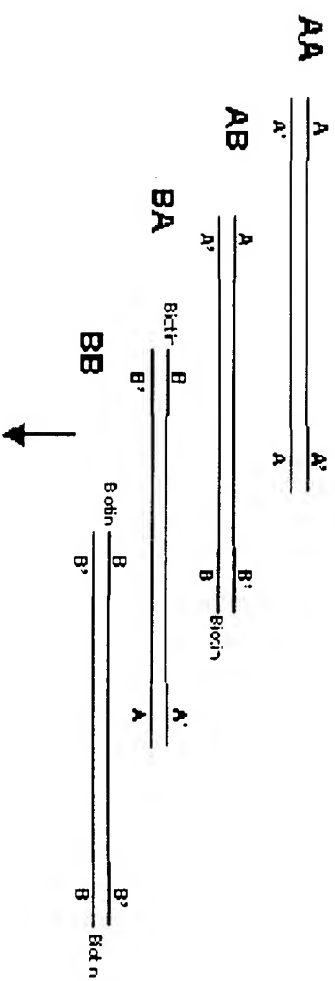


Figure 3

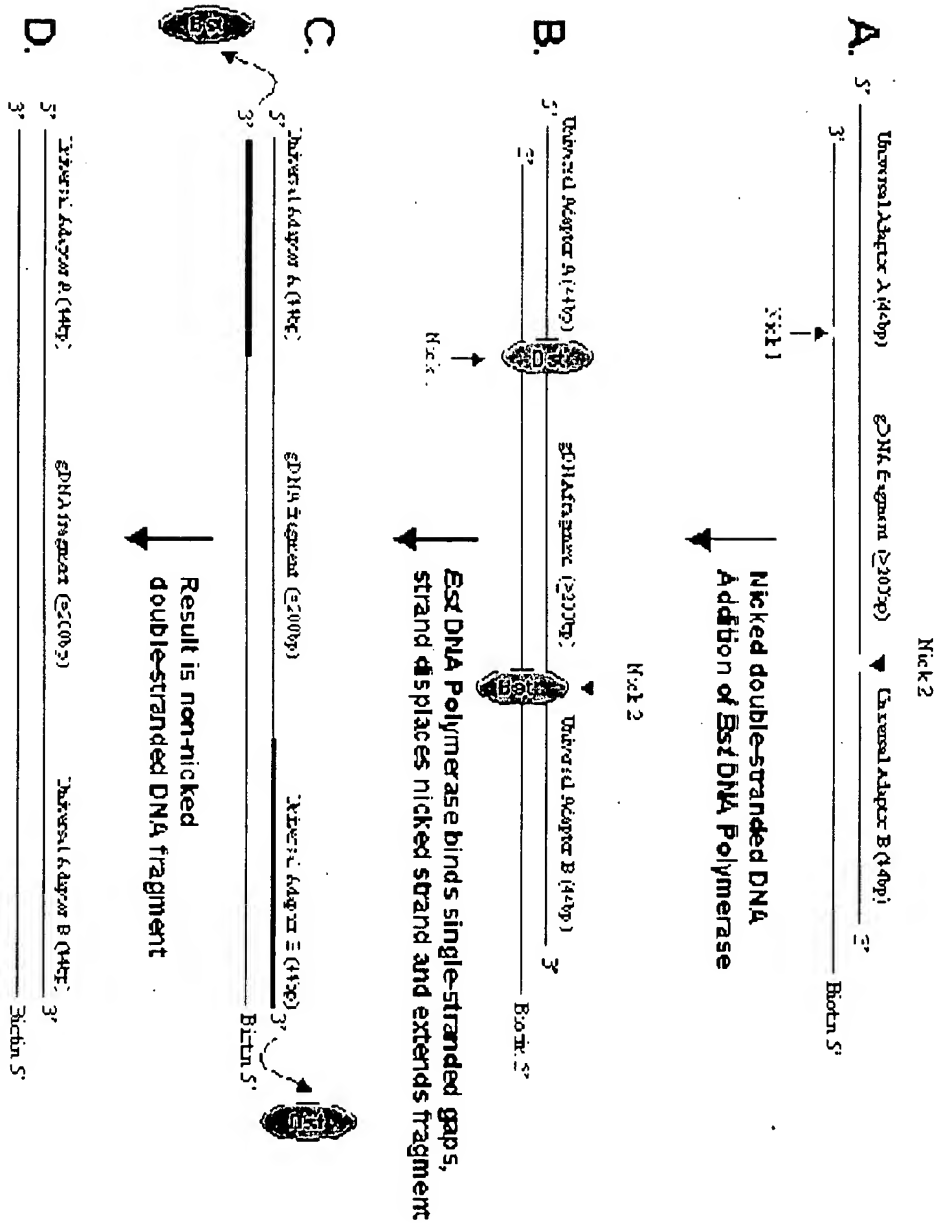


Figure 2A

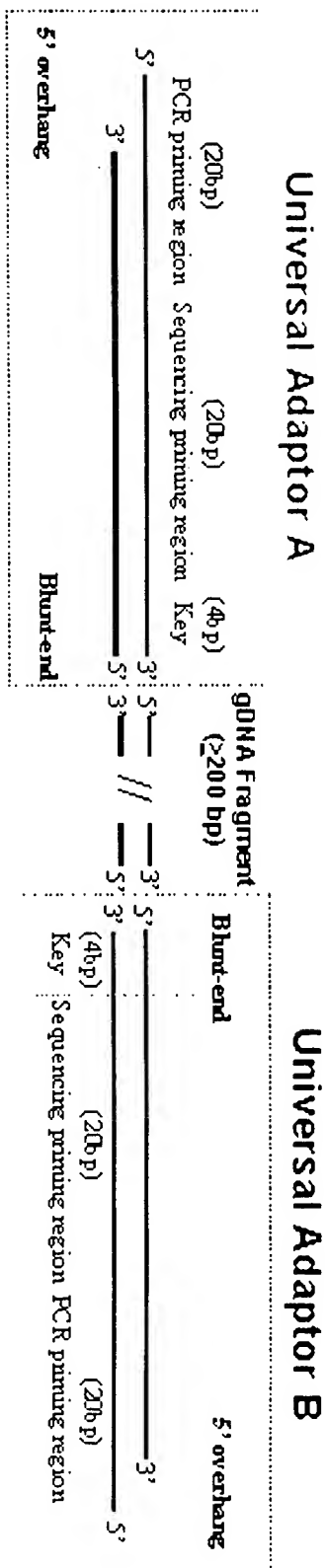


Figure 2B

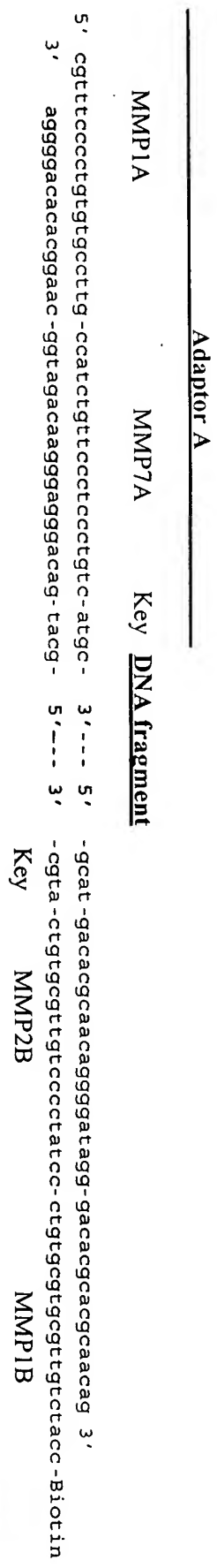


Figure 2C



## The 454 Sequencing system

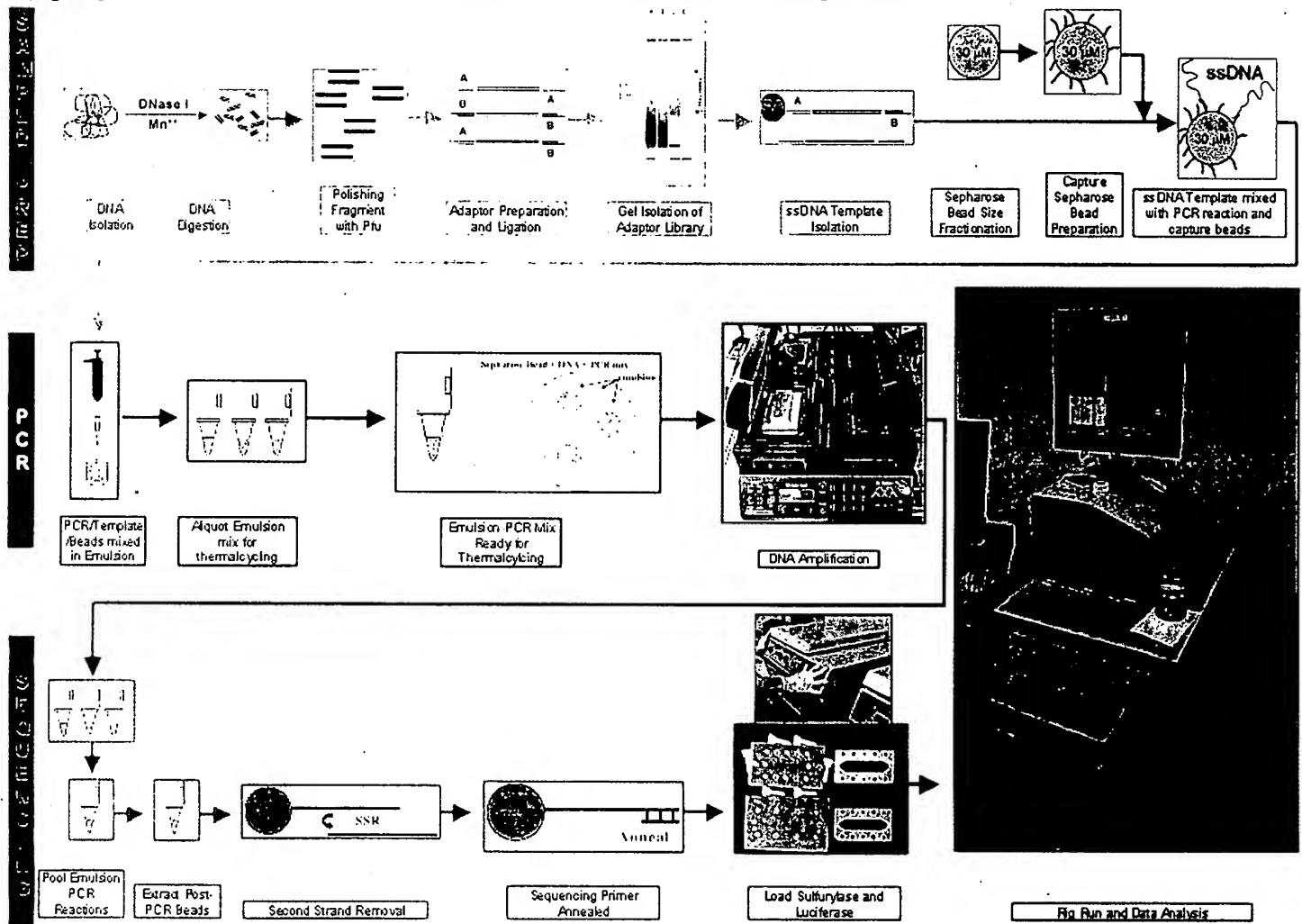


Figure 1 61

Figure 1F

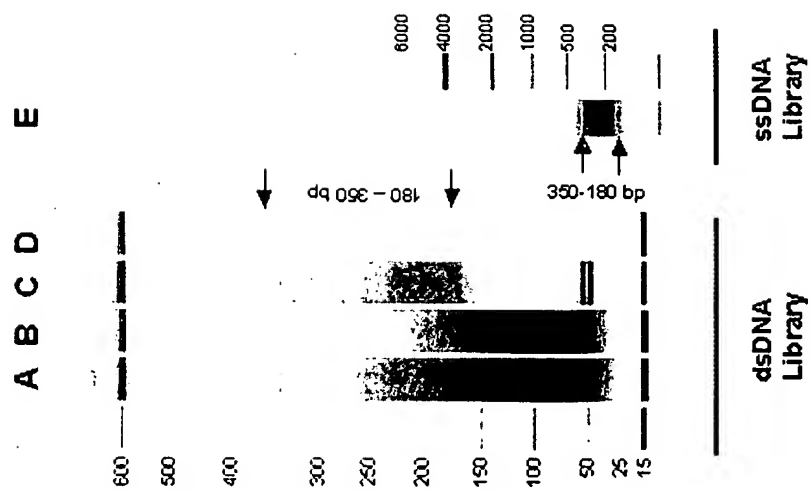




Figure 1A.

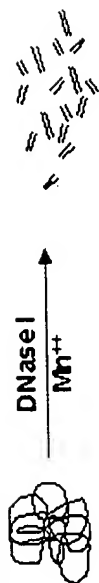


Figure 1B.



Figure 1C.



Figure 1D.

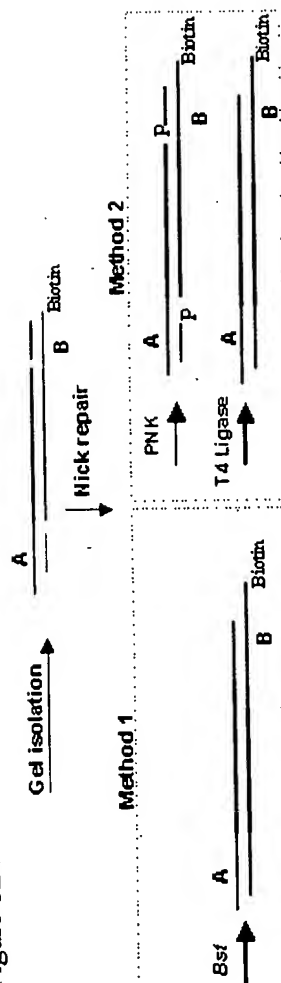
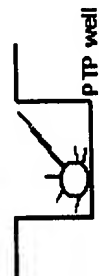


Figure 1E.

Bind non-nicked dsDNA to streptavidin-coated beads and single strand elution

Bind to Sepharose DNA Capture Bead (1 ssDNA per bead)

Deposition of a single DNA Capture Bead per well



Amplification  
Sequence